



1 TCG ACT ATG AAT GAT AAG GGT CCA ACA 31 TCT TGT CCT TCC ATA TCT TCC CAG AAC  
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asp

61 TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GGC AGC ATG TTC GAT CGG ACT TCC  
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

121 151 Cadherin  
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC  
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181 211  
CTG GAT GCC GAA GGG GAA GGA ATC ASC SAA GTA CAA AGG AAA GCT CTC AGT GCA ATT CAC  
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241 271  
AGC CTG CTA AGT TCT CAC CAC CTG GAC CCA GGC TGT GTC AAA CCA GAG CTG AAG GTC AAA  
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301 331  
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT  
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361 391  
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA  
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421 451  
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG  
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

481 511  
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG  
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541 571  
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC  
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601 631  
CTC ATT AGG AAG TGG ATT GGT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA  
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661 691  
TTT TTT ATT TTT CTG TTA TTT TTT GAT TAT AAA GAA AAA TAA AAT TTT GAT AAA CTC AAT  
leu phe ile cys val leu cys phe gln tyr lys gly lys gln ser ser asp lys val ser

721 751  
ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GGT TTG CTG CGT  
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

781 811  
GGG GAA GGG GGT AGA GGG GAG AAG ATG GCG TGC CGG GGT CTA GGG AAG GAT CGA TTT CTA

FIG. 1 (1 of 5)

901  
 AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT  
 lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala  
 911  
 ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT  
 thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala  
 1021  
 CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC  
 leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn  
 1081  
 TGT GAT CAG AGT ACC ACC TAC CTG ACT CAG TGC TTT GCA ACA CTC CGT GCT CTC ATC GCG  
 cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala  
 1141  
 AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAG CAA  
 lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln  
 1201  
 GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC GCG AGC CAA GCC TGT GCC ACC GCT  
 val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu  
 1261  
 TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATC CAA  
 tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln  
 1321  
 GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG  
 val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu  
 1381  
 AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT  
 arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr  
 1441  
 CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA  
 pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr  
 1501  
 GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT  
 val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile  
 1561  
 GAT AAG AAT TAT TAA GAA TTT TTT GAT CTA GAT TTA ATT TTT CTC TAA AAT ATG GAA GAG  
 asp lys asp tyr ala ala leu pro asp leu asp leu thr tyr leu ala asp met ala ile  
 1621  
 AAG CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCC GCT GCG  
 lys his thr lys lys lys cys tyr thr glu ala ala met cys leu val his ala ala ala  
 1681  
 TTA CTG GAT GAG TAT CTA AGT ATG TTA GAG GAG GAG AGT TAC CTC ACC CTG GCG AGT GTC  
 leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val  
 1741  
 TTA CTG GAT GAG TAT CTA AGT ATG TTA GAG GAG GAG AGT TAC CTC ACC CTG GCG AGT GTC  
 leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val  
 1801  
 TTA CTG GAT GAG TAT CTA AGT ATG TTA GAG GAG GAG AGT TAC CTC ACC CTG GCG AGT GTC  
 leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val

FIG. 1 (2 of 5)

1861 1891  
CTC CTC GAG CAG GGC GCG GAG CTC TTC AGC AGC GGA GGC TTA TAT GAG ACA GTT AAT GAG  
leu leu glu gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu

1921 1951  
GTC TAC AAG CTC CTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGS AAG CTG AIA CTC  
val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu

1981 2011  
ACT CAC AGC AAG CTG CAG AGA GGC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG  
thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met

2041 2071  
TTT GCA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GGG GAT ITG SAT GAA CAG  
phe gly thr tyr phe arg val gly phe phe gly ser lys phe gly asp leu asp glu gln

2101 2131  
GAG TTT GTC TAC AAA GAG CTT GCA ATT ACC AAG CTT CCF GAG ATC TCA CAT AGA CTA GAG  
glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu

2161 2191  
GMA ITT TAT GGI CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA SAC TCC ACT CCT  
ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro

2221 2251  
GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GGC TAC ATA CAG ATC AAT TTT GTG GAG CCC  
val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro

2281 2311  
TAT TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAT TTT GAG AAG AAT TTC AAC CTC  
tyr phe asp glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu

2341 2371  
GTT AGG TTC ATG TAC ACC AGC CGC TTC ACC CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT  
arg arg phe met tyr thr thr pro phe thr leu glu gly arg pro arg gly glu leu his

2401 2431  
GAG CAG TAC AGA AGG AAT ACA GTC CTC ACC ACT ATG CAC GCC TTC CAC TAC ATC AAG ACC  
glu gln tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr

2461 2491  
AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA  
arg ile ser val ile gln lys glu glu phe val leu thr pro ile glu val ala ile glu

2521 2551  
XX  
GTC ATG AAG AAG AAG AAT CTA CAG TTA GGA GTT GGT ATT AAT CAG GAG GCG GGT GAT GGA  
glu met leu lys leu thr thr thr thr leu ala val ala ile asn ala ala pro pro asp ala

2581 2611  
XX  
AAG ATG CTT CAG ATG GTG CTC CAA GGC TCT GTS GGA GCT ACT GTA AAT CAG GGA CCA CTG  
lys met leu gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu

2641 2671  
GAA GTA GTC CAA GCG TTT TTS GGT GAA ATT GCT GGT SAT GGA AAA CTC TAT CGA CAT CAC  
glu val ala ala val phe leu ala ala ile pro ala asp pro lys leu tyr arg his his

2701 2731  
GAA GAA TAT TAT AAT AAT TTA TAT TA AAT TAT TAT TA TAA TTT AAA AA AAT TAT  
glu lys arg leu ala thr thr thr thr thr thr thr thr thr thr thr thr thr thr thr thr

FIG. 1 (3 of 5)

XX  
 AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CCG AAA ATT CCA GAA CTG TAC AAG  
 asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys  
  
 1881 2811  
 TCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAT TCC TTC CAG AGA TCT AAT TTC AAG AAA  
 pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys  
  
 2941 2971  
 TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG  
 cys glu thr glu leu ser gln gly ser CCH glu lys pro ser ser phe val glu thr val  
  
 1001 1031  
 GCC CTG CAA CCC TGG AGA AGG AAT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG  
 ala leu gln pro trp arg arg thr cys trp tyr leu lys asn gly thr phe ala thr gln  
  
 1061 1091  
 GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA  
 asp STP  
  
 1121 1151  
 TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG  
  
 1181 1211  
 GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC  
  
 1241 1271  
 AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA  
  
 1301 1331  
 TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA  
  
 1361 1391  
 AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC  
  
 1421 1451  
 TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA  
  
 1481 1511  
 AAA TCA TCA TGC TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA  
  
 1541 1571  
 ATG GTG GAG CAA TTT CTG TAT AGT TAT TTT TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA  
  
 1601 1631  
 TAT GAA TTT ATA GAA GAA TAT ATT CAA ATT ATT TAT GAA TGA GAT AAT TGT TAT TTG GAG  
  
 1661 1691  
 CAG TCA GGC AAA AAT CAC AGA TAC TGC TTT CAC TTA AAT GGA AAC AAT TCT CCG ATA ATG  
  
 1721 1751  
 CTT TGC TTT TTT TTT TAT GTC ACT CTT GTG TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA  
  
 1781 1811  
 AAT TTT TTT TTA TAA AAT AAT AAT ATT TTT TTT ATT TTA GAA CAT TGT GGT GTG TGT

FIG. 1 (4 of 5)

4021  
AAC TCG

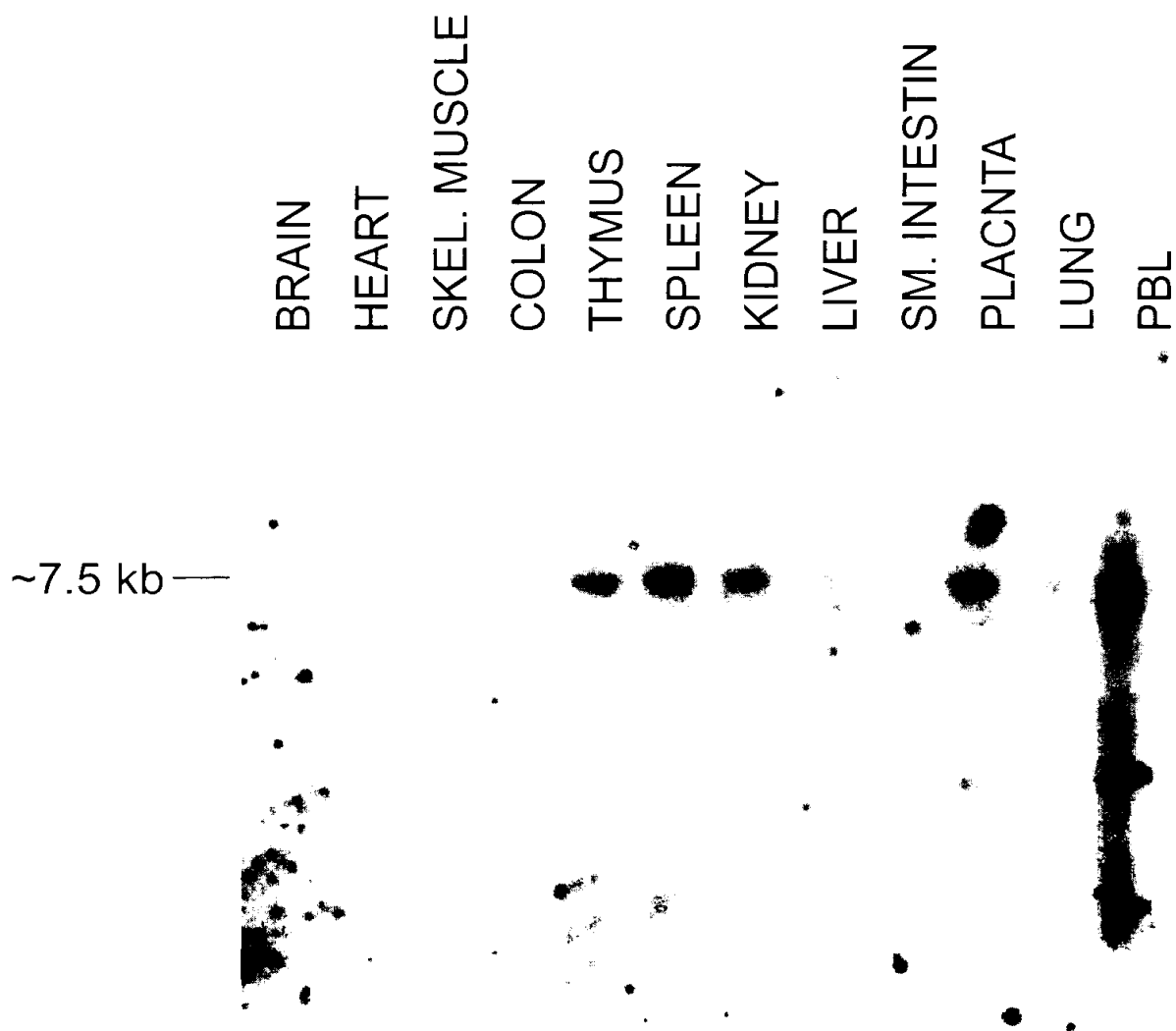


FIG. 2A

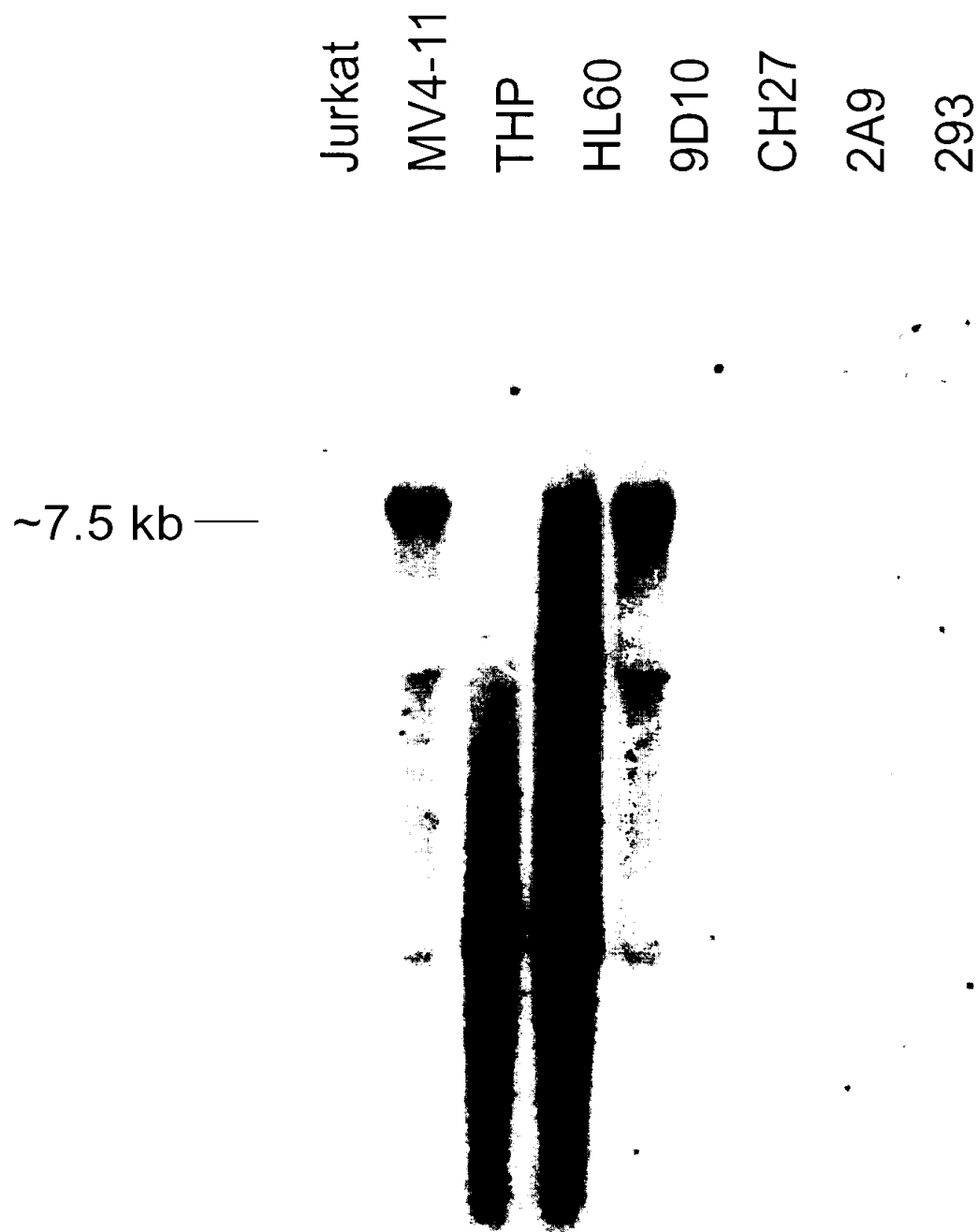


FIG. 2B

HC2A -----  
 KIAA ASGNLEKNARFSAIYRQDSNKLSNDOMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD  
 rat -----  
 HC4 -----  
 HC1 -----  
 HC3 -----  
 HC5 -----

HC2A -----  
 KIAA FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ  
 rat -----  
 HC4 -----  
 HC1 -----  
 HC3 -----  
 HC5 -----

HC2A -----VLHHQ(NPEFYDEIK  
 KIAA KSFARKARNIAICIEFKDSDEEDSQPLFCIYGRFGGPVFTRSFAFAVLHHQ(NPEFYDEIK  
 rat -----  
 HC4 -----  
 HC1 -----  
 HC3 -----  
 HC5 -----

HC2A IELPTQLHEKHALLLTFFHVSCDNSSFGSTKKEDVVETQVGYSWLPLLPDGRVVTSEQHI  
 KIAA IELPTQLHEKHALLLTFFHVSCDNSSFGSTKKEDVVETQVGYSWLPLLPDGRVVTSEQHI  
 rat -----  
 HC4 -----  
 HC1 -----  
 HC3 -----  
 HC5 -----

HC2A PVSANLPSGYLGYQELGMGFHYGPEIFWVDGGKPELLKISTHLVSTVYTQDCHLNFFQYC  
 KIAA PVSANLPSGYLGYQELGMGFHYGPEIFWVDGGKPELLKISTHLVSTVYTQDCHLNFFQYC  
 rat -----  
 HC4 -----  
 HC1 -----  
 HC3 -----  
 HC5 -----

HC2A QTESSAQALNELVKYKSLHAMEGQVMAFLPTILNQLEFVLT-RATQEEVAVNVIRV  
 KIAA QTESSAQALNELVKYKSLHAMEGQVMAFLPTILNQLEFVLT-RATQEEVAVNVIRV  
 rat -----  
 HC4 -----MEIQVLIRFLSVILMQLEFWVLPNMIHEIDVPISCQMV  
 HC1 -----MSFLPIILNQLEKVLV-QNEEDEITTTVIRV  
 HC3 NRSRLSNSNFDISGTFTSPDDEVRSIIIGSKGLDRSNGWVNTGGPKAAPWGSNPSPSAES  
 HC5 -----

FIG. 3A (1 of 5)



HC2A	11HVVAQCCHEEGLSHLSYVHYAYKAEPYVASEYKTVHEELTKSMTTILHPSADFLT'SN
KIAA	11HVVAQCCHEEGLSHLSYVHYAYKAEPYVASEYKTVHEELTKSMTTILHPSADFLT'SN
rat	-----
HC4	LFHIVSKCHEEGLDSYLSSFIHYSFRPGKPSAPQAPLIHETLATMMIALLIQSADFLAIN
HC1	LPDIYAKCHEEQLDHSVQSYIIFVPETR---ACKERPVEDLAKNVGTGLIH-SNDSPTVK
HC3	TQAMPDSNRMSSHTETISFLQTLTGRIIP---TKKLPHEELALQWVVCSSG---SVE---E
HC5	-----
	Cadherin Cleavage
HC2A	KLLRYSWFFFDVLIHSMAGHLIENSEVELIENQRFPAHYHHAETVVMMLMPHITQKFGD
KIAA	KLLRYSWFFFDVLIHSMAGHLIENSEVELIENQRFPAHYHHAETVVMMLMPHITQKFRD
rat	-----
HC4	KLLRYSWFFFEIIAHSMATYLLLEENKIELTSGQRFPAHYHHAELSLFLAIE-IYHSQYAE
HC1	HVLHRSWFFFAIILHSMAGHLIDTNKIQLEHPQRFPSYQNELDNLVMVLSDEYVWYKRD
HC3	SALQQAWFFFEIMVFSMTVHLLYFNDKLEAFKSRFPFLFMDDIAALVSTIASDVSFLQK
HC5	-----
HC2A	NPEASKNANHSLAVFTHRCFTFMDRGVFFQIN---NYIS--CHAPGDPKTLSEYHFLFL
KIAA	NPEASKNANHSLAVFTHRCFTFMDRGVFFQIN---NYIS--CHAPGDPKTLSEYHFLFL
rat	-----
HC4	1PKESRNVNYSLAGFLHCLTLMDRGFVFNLIN---DYIS--GFSPLHPEVLAHYFLFL
HC1	ALKEETRRATHSVARELHRCFTFMDRGCVFFMVN---NYIS--MFESGLIKETLCQYFFDEL
HC3	DTEMVERLNTSLAFELNLLSVMDRGFVFSLIKSCYKQVSSKLYSLNPVSVLVSLFLDEL
HC5	-----
HC2A	RVVCNHEHYIPLNLFM-----FFGEGRIQF-----YQDLQL----DYSITDEF
KIAA	RVVCNHEHYIPLNLFM-----FFGEGRIQF-----YQDLQL----DYSITDEF
rat	-----
HC4	QTICNHEHYIPLNLFM-----AFAPPKIQF-----YQDLHL----EYISLEY
HC1	QEVQCHEHFIPLCDFIRSANIFDPIFSES-----TQLHASEMPEYFVTFEF
HC3	RITCSHEHYVCLNLFPSCLTPPASFSPVSSATSQSSCFSTNVQDQIASMFELS--VVF
HC5	-----MMADTAFTSFCHSIS---SQNSLSCSSHQDQIASMFDRTSFVFA
	Cadherin EC motif
HC2A	CRNHFLVGLLRLVGTALQEFFRE---VRLIAISVLNLLIKHSFDQRYASRSHQARIAT
KIAA	CRNHFLVGLLRLVGTALQEFFRE---VRLIAISVLNLLIKHSFDQRYASRSHQARIAT
rat	-----
HC4	CRNHFLVGLLRLVGTALQEFFRE---VRLIAISVLNLLIKHSFDQRYASRSHQARIAT
HC1	CRNHFLVGLLRLVGTALQEFFRE---VRLIAISVLNLLIKHSFDQRYASRSHQARIAT
HC3	CRNHFLVGLLRLVGTALQEFFRE---VRLIAISVLNLLIKHSFDQRYASRSHQARIAT
HC5	CRNHFLVGLLRLVGTALQEFFRE---VRLIAISVLNLLIKHSFDQRYASRSHQARIAT
HC2A	LYLPLFGLLIENVQRINVRDVSPPFNAG-MTVKDESALALPANNPLVTPQKGSTLDNSLH
KIAA	LYLPLFGLLIENVQRINVRDVSPPFNAG-MTVKDESALALPANNPLVTPQKGSTLDNSLH
rat	-----
HC4	IYIIFVGLLENIPLAGRTLYSCAAMPNCAARDEEPFGS-----FTSF--AN--EGSLS
HC1	IYIIFVGLLENIPLAGRTLYSCAAMPNCAARDEEPFGS-----FTSF--AN--EGSLS
HC3	IYIIFVGLLENIPLAGRTLYSCAAMPNCAARDEEPFGS-----FTSF--AN--EGSLS
HC5	IYIIFVGLLENIPLAGRTLYSCAAMPNCAARDEEPFGS-----FTSF--AN--EGSLS

FIG. 3A (2 of 5)

HC2A KELLGATSGIASPYTTSTFNINSURNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS  
 KIAA KELLGATSGIASPYTTSTFNINSURNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS  
 rat -----  
 HC4 TDKDTAYGSEFQNS-----HGIKREDGRSLIP-EGATGFPDQGNITGEN-----TRQS  
 HC1 EDVLNBIAAEFSE-----IAISFNHACDHASHASLDGNPITNFKSSEKICNCEKIPRSL  
 HC3 QIVAMAIAGTSVI-----LTAPGSEFLTSTSTSRQHT-----  
 HC5 QNVALAIAQNNFN-----LKTSG-IVLSSLPVHCYN-----

HC2A TLGNSVVAQDKLDQSEIKSLLMDFLYILKMSDDALFTYWN-KASTSELMDFFETISEVCL  
 KIAA TLGNSVVAQDKLDQSEIKSLLMDFLYILKMSDDALFTYWN-KASTSELMDFFETISEVCL  
 rat -----  
 HC4 STRSSVQQYNRLDQVEIRSLIMDFLYIVHMISEDTLLTYWN-KVSPQELINILILIEVCL  
 HC1 ALIGSTPLFPDRLDQAEATRSLLMDFLRIMKTSYETLIAYWJ-RAPSPPEVSDFFSILDVCL  
 HC3 -----TFSAESSRSLLDCLLVLMKN-ADETVLQKWFTDLSVLQLNRLDPLIYLV  
 HC5 -----MINADPTRNLMDFLWIMKN-ADQSLRKWIADLPSTQLNRLDPLIYLV

HC2A HQFQYMGFYIAFMQEGLG--PIVHRRFS-----QTLPVSENETGM  
 KIAA HQFQYMGFYIAFM-----TGMM  
 rat -----  
 HC4 FHEFIMGFYIAFMHDAWLSKHFGLDRFS-----LTMPALNFSGYM  
 HC1 QNFEVLDGHEFIIEHIAAAF--EFVQSTQNDSTLKGSNPSCQTSGLLAQWHESTIRHEGHE  
 HC3 SCFEVHGFYEFERINSLTEK--KSPKMAAF-----DEEALGSGIGAFQEMV  
 HC5 LCFEYHGEQSSDFVSTQVLQ--KSEVWFAE-----LEEALLRGEQAFGEMM

HC2A HAELQQL-----GSLDHS-----LTFNHSYGHVDAVLEHQSLLEANIATEVC  
 KIAA HAELQQL-----GSLDHS-----LTFNHSYGHVDAVLEHQSLLEANIATEVC  
 rat -----  
 HC4 QAEHQHL-----SSLEDS-----FTLNHSSTITEADIFHQALDEGNTATEVC  
 HC1 QHESQTHIIRGF---NALSINPIL---IQMLICITMTSNBNEIDGVHHVDTREANIATEGC  
 HC3 RRSEHQLEFSPSGLAFGSQENLWFFDMTHWRQNTKLDKFAEIEHEALIDGNLATEAN  
 HC5 RREAFGNHFFP-----GLNENLWFFDQTHWRQANEKLDKFAELDQEALEGNLATEAN

HC2A LTALQTLSEFTLAFENQLLADHGHELMHFVEIVYLQFLQHQSEETALKNVFTALESLIY  
 KIAA LTALQTLSEFTLAFENQLLADHGHELMHFVEIVYLQFLQHQSEETALKNVFTALESLIY  
 rat -----  
 HC4 LTVLQTLSEFTQCFKTHFLNNDGHELMHFVEIVYLQFLQHQSEEMALKNVFTALESLIY  
 HC1 LTILQTLSEFTQTHQRQLQQDCQNSLHKGFELTYMLFFQVQNSATALKHVFALEFLFVC  
 HC3 LIILQTLSEIVVQTVS--VTEA--RESILGGVLEVLLHSMANQSAVYLQHFATQRAIMV  
 HC5 LIILQTLQENIQASG--ALDC--KDSILGGVLEVLVNSLNCQSCCTVTHQFATLRALIA

HC2A KFFSTTEYQRAIMAAALVEYLEDGNSHLSNITEASQLIFLMPIHNFYTGKSEVITH  
 KIAA KFFSTTEYQRAIMAAALVEYLEDGNSHLSNITEASQLIFLMPIHNFYTGKSEVITH  
 rat -----  
 HC4 KFFSAFFQGRVNMAAFCYEVLECCTSISSTNEASALLVLLMRNPFYTKKHTFLKTH  
 HC1 KFFSAFFQCPADLGSCFCYEVLECCNHSESTQTEASALLVLMRNPFYTKKQKSVITH  
 HC3 KFPDLLFEEETECCADLCRLIRHCSSSIGTIRHPSASLVLLMRQNFTEGN--NFARVK  
 HC5 KFGDLLFEEEVQCFDLCHQVLLHCSSSMDVTEIQCACATLYLLMRFSFGATS--NFARVK

HC2A LQVITSVSQLIADVVGIGETRFQSLGIINNCANSDRLIRHTSFSSDVKDLTHERIRTVIM  
 KIAA LQVITSVSQLIADVVGIGETRFQSLGIINNCANSDRLIRHTSFSSDVKDLTHERIRTVIM  
 rat -----

HC2A LQVITSVSQLIADVVGIGETRFQSLGIINNCANSDRLIRHTSFSSDVKDLTHERIRTVIM

FIG. 3A (3 of 5)

Transmembrane

HC2A    ATAQMKERENDPEMLVDLQYSLAKSTASTPELRKTWLDSEAKIHVKNQDLSEAAACGYVHV  
KIAA    ATAQMKERENDPEMLVDLQYSLAKSTASTPELRKTWLDSEAKIHVKNQDLSEAAACGYVHV  
rat    ATAQMKERENDPEMLVDLQYSLAKSTASTPELRKTWLDSEAKIHVKNQDLSEAAACGYVHV  
HC4    ATAQMKERENDPEMLVDLQYSLAKSTASTPELRKTWLDSEAKIHVKNQDLSEAAACGYVHV  
HC1    ATAQMKERENDPEMLVDLQYSLAKSTASTPELRKTWLDSEAKIHVKNQDLSEAAACGYVHV  
HC3    DTVMHLEHQEDPEMLIDLMYRIAKGPTQSPDLRLTLWLQNIAGHSHERSNHAEAAACLVHS  
HC5    DTVMHLEHQEDPEMLIDLMYRIAKGPTQSPDLRLTLWLQNIAGHSHERSNHAEAAACLVHS

SH3

HC2A    TALVAEYLTRKGV-----FAQSGTAFVMTIN  
KIAA    TALVAEYLTRKGV-----VQWERPLLPRSHSALRRSGSGVTEQSGTAFVMTIN  
rat    TALVAEYLTRKGV-----LALQREPPVPPSHTSQCKKSGSGVTEQSGTAFVMTIN  
HC4    AALVAEFLTRKGL-----FENGCSTAFVMTIN  
HC1    AALVAEFLTRKGL-----FENGCSTAFVMTIN  
HC3    AALVAEFLTRKGL-----RHYLGVSGVTEQSGTAFVMTIN  
HC5    AALVAEFLTRKGL-----HSYLVGVSGVTEQSGTAFVMTIN

ITAM

HC2A    IDEEASMMLEVMQD-----VHFNEIWLMELELADGLWFAEFLIADIYPLI  
KIAA    IDEEASMMLEVMQD-----VHFNEIWLMELELADGLWFAEFLIADIYPLI  
rat    IDEEASMMLEVMQD-----VHFNEIWLMELELADGLWFAEFLIADIYPLI  
HC4    IDEEASMMLEVMQD-----VHFNEIWLMELELADGLWFAEFLIADIYPLI  
HC1    IDEEASMMLEVMQD-----VHFNEIWLMELELADGLWFAEFLIADIYPLI  
HC3    IDEEASMMLEVMQD-----VHFNEIWLMELELADGLWFAEFLIADIYPLI  
HC5    IDEEASMMLEVMQD-----VHFNEIWLMELELADGLWFAEFLIADIYPLI

ITAM    ITAM    ITAM    ITAM

HC2A    YEKHEDFELARLITTHRAYSMTVMHSGRALLVTFEFAFFGQAAQYQPTI  
KIAA    YEKHEDFELARLITTHRAYSMTVMHSGRALLVTFEFAFFGQAAQYQPTI  
rat    YEKHEDFELARLITTHRAYSMTVMHSGRALLVTFEFAFFGQAAQYQPTI  
HC4    YEKHEDFELARLITTHRAYSMTVMHSGRALLVTFEFAFFGQAAQYQPTI  
HC1    YEKHEDFELARLITTHRAYSMTVMHSGRALLVTFEFAFFGQAAQYQPTI  
HC3    YEKHEDFELARLITTHRAYSMTVMHSGRALLVTFEFAFFGQAAQYQPTI  
HC5    YEKHEDFELARLITTHRAYSMTVMHSGRALLVTFEFAFFGQAAQYQPTI

ITAM    ITAM

HC2A    -FFFEDEEGHEIYHKEFLTPLEISQALLKESDRFGSENVNIIQDSGVNIIHLSKTA  
KIAA    -FFFEDEEGHEIYHKEFLTPLEISQALLKESDRFGSENVNIIQDSGVNIIHLSKTA  
rat    -FFFEDEEGHEIYHKEFLTPLEISQALLKESDRFGSENVNIIQDSGVNIIHLSKTA  
HC4    -FFFEDEEGHEIYHKEFLTPLEISQALLKESDRFGSENVNIIQDSGVNIIHLSKTA  
HC1    -FFFEDEEGHEIYHKEFLTPLEISQALLKESDRFGSENVNIIQDSGVNIIHLSKTA  
HC3    -FFFEDEEGHEIYHKEFLTPLEISQALLKESDRFGSENVNIIQDSGVNIIHLSKTA  
HC5    -FFFEDEEGHEIYHKEFLTPLEISQALLKESDRFGSENVNIIQDSGVNIIHLSKTA

ITAM

HC2A    YIQVTHVITFFDEKEIQRKTEFERCHNIRLEMFEMPIQTGTGFAQGGVIEQCHITILTA  
KIAA    YIQVTHVITFFDEKEIQRKTEFERCHNIRLEMFEMPIQTGTGFAQGGVIEQCHITILTA  
rat    YIQVTHVITFFDEKEIQRKTEFERCHNIRLEMFEMPIQTGTGFAQGGVIEQCHITILTA  
HC4    YIQVTHVITFFDEKEIQRKTEFERCHNIRLEMFEMPIQTGTGFAQGGVIEQCHITILTA  
HC1    YIQVTHVITFFDEKEIQRKTEFERCHNIRLEMFEMPIQTGTGFAQGGVIEQCHITILTA  
HC3    YIQVTHVITFFDEKEIQRKTEFERCHNIRLEMFEMPIQTGTGFAQGGVIEQCHITILTA  
HC5    YIQVTHVITFFDEKEIQRKTEFERCHNIRLEMFEMPIQTGTGFAQGGVIEQCHITILTA

FIG. 3A (4 of 5)

Coiled-Coil 1

HC2A	IHCFPVYFRIPVVMYQHHTDLNPIEVAIDEMSRKVAELRQLCSSAEVVMIRLQLQLQSSV
KIAA	IHCFPVYFRIPVVMYQHHTDLNPIEVAIDEMSRKVAELRQLCSSAEVVMIRLQLQLQSSV
rat	IHCFPVYFRIPVVMYQHHTDLNPIEVAIDEMSRKVAELRQLCSSAEVVMIRLQLQLQSSV
HC4	SNSEFYFRIPINCEQQINLKEPIDGATTELRKTAELQKLCSFVDMIQQLQLQSSV
HC1	SHLFPYFKKRIQVISQSSTELNPIEVAIDEMSRKVSLELNQLCTNEEVIMISLQLQLQSSV
HC3	SHAPFYKTRVNVTHKEEIIILTPIEVAIEDMQFKTQELAFATHQDPADPKNLMQVQLQSSV
HC5	MHAPFYKTRISVIQKEEFVLTPIEVAIEDMFKTQLQAVAINQSPDAKNLMQVQLQSSV

Coiled-Coil 2

HC2A	SVQVNAGPLAIAAFELDDTNTRYPDNKVLLLEVFQFVEACGQALAVNERLIFEDQLE
KIAA	SVQVNAGPLAIAAFELDDTNTRYPDNKVLLLEVFQFVEACGQALAVNERLIFEDQLE
rat	SVQVNAGPLAIAAFELDDTNTRYPDNKVLLLEVFQFVEACGQALAVNERLIFEDQLE
HC4	SVQVNAGPLAIAAFELNDSQASHYPPKKVSELDNFKFIQACSIALELNEFLIFEDQVE
HC1	SVQVNAGPLAIAAFLEETNAKHYPDNQVLLLEIFQFADACGQALIVNEFLIFEDQLE
HC3	SVTVNQGLEVAQVFLSEIPSDPHLFRHHNKLELCFFDFTRCEDALEKNSLIGPVQFE
HC5	SVTVNQGLEVAQVFLSEIPADPHLYFRHHNKLELCFFEFINRCGEAVEKNFLITAQFE

Coiled-Coil 2

HC2A	YQEEHMFANYEEMAKELSEIMHEQIQCLEEETTS-VLPNSLHIFNAISGTPSTMVHGMTSS
KIAA	YQEEHMFANYEEMAKELSEIMHEQQLG-----
rat	YQEEHMFANYEEMAKELSEIMHEQIQCLEEETTS-VLPNSLHIFNAISGTPSTMVHGMTSS
HC4	YQEEHMFANYEEMAKELSEIMHEQIQCLEEETTS-VLPNSLHIFNAISGTPSTMVHGMTSS
HC1	YQEEHMFANYEEMAKELSEIMHEQIQCLEEETTS-VLPNSLHIFNAISGTPSTMVHGMTSS
HC3	YQEEHMFANYEEMAKELSEIMHEQIQCLEEETTS-VLPNSLHIFNAISGTPSTMVHGMTSS
HC5	YQEEHMFANYEEMAKELSEIMHEQIQCLEEETTS-VLPNSLHIFNAISGTPSTMVHGMTSS

PEM

HC2A	SVVV-----
KIAA	-----
rat	CVTLPHPEPHVGTCEVMCKLRRTTFANHWFCQAQEEAMGNGFEKEPWTVIFNSRFYFSWCK
HC4	EV-----
HC1	SAEV-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	-----
rat	VHIFF-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

FIG. 3A (5 of 5)

	A	B	
CLASP-1	YRVAFYGQ:::GFFFEEDGKEYIYKEP		
KIAA1058	FRVAFFGQAAQYQFTDSLTVESGPFEDDSKEYIYKEP		
CLASP-2	FEDEDGKEYIYKEP		
CLASP-6	FRVAFFGQ:::GFFFEEDGKEYIYKEP		
CLASP-4	FRVAFYGQ:::GFFFEEDGKEYIYKEP		
DOCK180	FAMGYYGQ:::GFTFLRGKVFYIRGHEYESPED		
DOCK2	FAMGYYGQ:::GFTSFLRNKVFYIRGHEYESPED		
DOCK3	FRMGFYGR:::HFFFLNHEYVWFGH		
KIAA0716	FRMGFYGR:::HFFFLNHEYVWFGH		
CLASP-3	FRMGFYGT:::HFGDLDEQEFYKEP		
CONSENSUS	F V FYG	FEL F	
	YF	Q F R	
			C
TRG	PKLTPLSEISQFLLELYSDKESENVEMLDSCGVNELLQSKFAXIQVTHVTPFFDEKE		
CLASP-1	PKLTGLSEISQFLLELYADKASNVETDQDNFVNELLQPKYANIQVTVTPFFEEKE		
CLASP-2	PKLTPLSEISQFLLELYSDKESENVEMLDSCGVNELLQSKYANIQVTHVIPFFDEKE		
CLASP-4	PKLTGLSEISQFLLELYGKFTENVETDQDNFVNELLQPKYANIQVTVVKPYFDDEKE		
CLASP-3	PAITFLAELHLEEGFYCHKEEDVVEVIKDSNELLQPLPNKAMIQITYVEPYFDITYE		
KIAA0716	HDYEFLEAFQCFMINEFFHATA-----MQHANQPIETFLAEAYLQIYAVTPIPEEQE		
DOCK3	HDYEFLEAFQCFMINEFFQATA-----MQHENHETIALQCDAYLQIYAVTPIPYVD		
DOCK2	FQMQLNTQFIDAK-----MNTTSAIGFDVFNAPGQYIQCFTVQPVLDDEHP		
DOCK180	EYERREDFQMQLNTQFPNAEK-----MNTTSAIGFDVFNAPGQYIQCFTVQPVLDDEHP		
CONSENSUS	L D Y		YIQ+ V P D
	M F		L E
	E	E	
CLASP-1	RTILTTSHTFFYVFRRIQVIGQSSSTELNPIEVAIDEMKFFVSELN		
TRG	RTILTAIHQFFYVFRRIIVNQHTDLNPIEVAIDEMKFFVAELN		
KIAA1058	RTILTAIHQFFYVFRRIIVNQHTDLNPIEVAIDEMKFFVAELN		
CLASP-2	RTILTAIHQFFYVFRRIIVNQHTDLNPIEVAIDEMKFFVAELN		
CLASP-6	RTILTAIHQFFYVFRRIIVNQHTDLNPIEVAIDEMKFFVAELN		
CLASP-4	RTILTTSNSFFYVFRRIINCEQQINLKTIDVATDELDFETAELO		
CLASP-3	RTILTTSHTFFYVFRRIIVNQHTDLNPIEVAIDEMKFFVAELN		
CLASP-5	NTVLITMHTFFYVFRRIISVIQHEEFVLTPIEVAIDEMKFFTLQLA		
KIAA0716	RTSLYLVSQSLPGISRWFEVKKVEMSLLENALIEVLENKNNQQLK		
DOCK3	RTSEVTAYKLPGLRWFEVEMSQTTISLENALIEVLENKNNQQLK		
DOCK2	RTTITLTHNLESTIRWFEVEMSQTTISLENALIEVLENKNNQQLK		
DOCK180	RTSEVTAYKLPGLRWFEVEMSQTTISLENALIEVLENKNNQQLK		
CONSENSUS	RT L EP V + V + + E AI + M + L		
	F L I		

FIG. 3B (1 of 2)

CLASP-1	SLQLKLQSSVSVKVNAGPMANARAFLEETNARKYPDNQV--KLLLEIFRQFADACGGQALD
TRG	KLQLKLQSSVSVQVNAGPLANARAFLLDDTNTFRYPDNKV--KLLLEIFRQFVEACGGQALA
KIAA1058	KLQLKLQSSVSVQVNAGPLANARAFLLDDTNTFRYPDNKV--KLLLEIFRQFVEACGGQALA
CLASP-2	KLQLKLQSSVSVQVNAGPLANARAFLLDDTNTFRYPDNKV--KLLLEIFRQFVEACGGQALA
CLASP-6	KLQLKLQSSVSVQVNAGPLANARAFLLDDTNTFRYPDNKV--KLLLEIFRQFVEACGGQALA
CLASP-3	MLQMVLQSSVGTITVNQGPLEVAQVELSE--IPSDPKLFFHHNKLLCFKDFTKRCEDALR
CLASP-4	QLQLKLQSSVSVQVNAGPLANARAFLLNDSQASFYPFKKVSLEKDNFKFT--QACSTALE
CLASP-5	MLQMVLQSSVGTITVNQGPLEVAQVELAE--IPADPKLYLHHNKLLCFKEFTMRCGEAVE
KIAA0716	PLTMCLNGVLDAAVNGGVSRQQAFFVKEYILSHPEDGKFIARLEELMLEQAQILEFGLA
DOCK2	PLSMLLNGIVDPVAVMGGFATLEKAFFTEEYVRIHPLEQDKLTHLRLIAWQIPFLGAGIK
DOCK3	LLSMCLNGVIDAAVNGGIAREQAFFFDKDYINKHFGDAEKITQLLELMQEQVHVLGVGLA
DOCK180	PLSMLLNGIVDPVAVMGGFATLEKAFFTEEYVRDHPLEAHEKIEKLELIAWQIPFLAEGTR
CONSENSUS	L M L+G V VN G Y AFL + + P L+ L
	L I W V F + I

DOCK2=KIAA0209  
DOCK3=KIAA0299  
CLASP2variant=KIAA1058

FIG. 3B (2 of 2)

ref 1.1 ↓

1 31  
TGG ACT ATG AAT GGT GAT ACT GGT CCA AAA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC  
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

41 61  
TTA AGT TTT TTT TTT ACC TTT CAG GAG CAG AAG ATC GTC AGC ATG TTT GAT CGG ACT TCC  
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

101 121  
AGA GTA GGC GGC AGC AGC ACT TCC TCA CCG GCG CTC CTC TTC ACA GAA CTG GCT GCT GGC  
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

161 181  
CTG GAT GGC GAA GGG GAA GGA ATC AGC GAA CTA CAA AGG AAA GCT GTC AGT GCA ATT CAC  
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241 261  
AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA  
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301 321  
ATC GGC GGC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT  
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361 381  
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC GGC ACC AGT GGC TCG GAT GAA GAA CAA GAA  
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421 441  
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG  
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

ref 2.1 ↓

481 501  
AAA ACA ACT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG  
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541 561  
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC  
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601 621  
CTC ATT AGC AAG TGG ATT GCT GAC CTG CCA CCA ACG CAG CTC AAC AGG ATT TTA GAT CTA  
leu ile asp lys trp ile ala asp leu pro thr gln leu asn arg ile leu asp leu

661 681  
CTT TT ATT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT  
leu phe ile cys val leu cys phe ala tyr lys gly lys gln ser ser asp lys val ser

721 741  
ATC GAA ATT TTT CAG AAG TCA AGC GAT CTC AAG GCC CGC CTC GAA GAG GCT TTG CTG CGT  
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

781 801  
TTT GAA GAA GAA GAA GAA GAA GAA GAA GAA GAA GAA GAA GAA GAA GAA GAA GAA  
leu gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa

FIG. 4A (1 of 7)

841 871  
 AGT CTA AAT GAA AAT TTS ASA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GGT AAT GAG  
 gly leu asp ala asp leu arg trp lys lys glu gln thr his trp arg gln ala asp gln

881 931  
 AAG CTA CAT AAA ATA AAG GGC GAG TTA CAT CAA GAA GGC TTG ATC AGT GGC AAT CTG GCT  
 lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala

941 991  
 AGA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT  
 thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala

1021 1051  
 CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC  
 leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn  
 ↓ ref 3.1

1061 1111  
 TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC  
 cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala

1141 1171  
 AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA  
 lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln

1201 1231  
 GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT  
 val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu

1261 1291  
 TAC CTC CTC ATG AGG TTC AGT TTT GGA GGC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA  
 tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln

1321 1351  
 GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG  
 val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu

1381 1411  
 AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT  
 arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr

1441 1471  
 TCT TTT GGC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA  
 pro pro pro thr gln val gln ala leu leu cys asn leu asn ser ile leu tyr asp thr

1481 1541  
 TTT AAA ATT AAT GAA TTT CAT GAA CAT CTT GAG ATT TTT ATG CAT CTC ATG TAT AGA ATT  
 val lys met arg ala pro gln gln asp pro glu met leu met asp leu met tyr arg ile

1561 1591  
 GTT AAG AGT TAC CAG GCA TTT CTT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG  
 ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala gln

1601 1641  
 AAA CAT AAT AAT AAT AAT TTT CAT AAT GAT CTT GAG ATT TTT ATG CAT CTC ATG TAT AGA ATT  
 leu ala thr leu leu leu leu leu ala ala met tyr leu val his ala ala ala

FIG. 4A (2 of 7)



1681  
TTA GTG GGT GAG TAT CTA ACC ATG CTG GAG GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC  
leu val ala ala tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val

1741  
AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG  
ser phe ala asn ile ser ser asn val leu glu glu ser val val ser glu asp thr leu

1801  
TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC  
ser pro asp glu asp gly val cys ala gly gln tyr phe thr glu ser gly leu val gly

1861  
CTC CTG GAG CAG GGC GCG GAG CTC TTC AGC ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG  
leu leu glu gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu

1921  
GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC  
val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu

1981  
ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG  
thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met

2041  
TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG  
phe gly thr tyr phe arg val gly phe phe gly ser lys phe gly asp leu asp glu gln

2101  
GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG  
glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu

2161  
GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT  
ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro  
↓ ref 4.1

2221  
GTC GAT AAA ACC AAC TTG GAT CTT AAC AAG GGC TAC ATA CAG ATC ACT TTT GTG GAG CCC  
val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro

2281  
TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC  
tyr phe asp glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu

2341  
TAC AAT TTT ATG TAT ACC ACC CTA TTT AAT TTT GAG GGT TTT CTT TCG GCA GAG ATG CAT  
tyr asn phe met tyr thr thr pro phe thr leu glu gly asp pro arg gly gln leu his

2401  
GAG TAC TAT AAA AAG AAC ACA CTC CTA AAT ACT ATG CAC GGC TTC CCC TAC ATC AAG ACC  
glu gln tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr

2461  
AAT ATT AAT TTT ATT TAT AAA GAT GAT TTT TTT TTT ATA TTT ATT GAA TTT TTT ATT GAA  
asn leu ser val ile ala lys ala ala phe val leu thr pro ile ala val ala ile ala

FIG. 4A (3 of 7)

2571 2581  
 GA<sup>+</sup> ATG AAG AAG AAG AAT GTG CAG TTA GCA GTT GTC ATT AAC CAG GAG GCG GGT GAT GGA  
 asp met lys lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala

2591 2601  
 AAG AAT TTT TAT ATG GAT TTT TAA GGT TTT GTG GGA ATT ACT GTA AAT CAG GGA GCA CTG  
 lys met leu gln met val leu gln gln met val gln ala thr val asp gln gly pro leu

2611 2621  
 GAA GTA GCC CAA GTG TTT TTG GGT GAA ATT GCT GGT GAT CCA AAA CTC TAT CGA CAT CAC  
 glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

2631 2641  
 AAC AAG TTT AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA  
 asp lys leu arg leu lys phe lys gln phe ile met arg cys gly glu ala val glu lys

2651 2661  
 AAC AAG CGT CTC ATC ACS GCA GAT CAG AGG GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT  
 asn lys arg leu ile thr ala asp gln arg glu tyr gln gln glu leu lys lys asn tyr

2671 2681  
 AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG  
 asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys

2691 2701  
 CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA  
 pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys

2711 2721  
 TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG  
 cys glu thr gln leu ser gln gln ser OCH

2731 2741  
 ref 5.1  
 GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG

2751 2761  
 GAC TGA CTG TAC ACT GCG TGA TCA GCG AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA

2771 2781  
 TGG AAT TAT TCG CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGG GGG ATG

2791 2801  
 GAG GAT GAG TAC TCA GCG ATG ACT GCG TAT TCA TTA AAG TGT GTT TTT CCA CAA TGT ACC

2811 2821  
 AAA CAA GGT ATA AAT AAT TTT TAT TTT TTA TTT GGT AAT TAT TAT TTA TGT GAG AGA TTA

2831 2841  
 TTT TAT GTT GGT TAT ATT TTA ATT TAT TTT AGT AAG TTA AAT TGT CTG AGG AAA AAT GGA

2851 2861  
 AAA ATT ATT CAC CAG TGG ATT CAA ACT GAA TTT CAC TCT TTA TAT GAA GGG AGG GCA AAC

2871 2881  
 TTA TAT GAG TAT GAA ATA TTT TTA ATA AAT TTA CAA AGG GAA TTT TTA TTA CAA TTT CAA

FIG. 4A (4 of 7)

3541  
 AAA TGA TGA TGG TTT GAA ATT TGG GAG GAG ATT ATT TGT GAA GTT GTT ACC GTT TTS GTA  
 3571  
 ATG GTG GAA TAA TTA GTG TAT AGT TAT TTT TGT TTT ATT ATT ATT GTT AGA TTA ATT TAA  
 3601  
 CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC ACT GAT GTA GGA GAT ACA CGG TAC TIG GAG  
 3631  
 CAG TCA GGC AAA AAT CAG AGA TAC TGG TTT CAC TTA AAT GGA AAC AAT TGT CCG ATA ATG  
 3661  
 GTT TGG TTT TTT TGT TAT GTG ACT GTT GTG TAC TAT CTA TTT TTC TCC TGT GTG GGA CCA  
 3691  
 AAT TTT TTT TTA TAA AGC AAT AAT ATG TCT GTT TTC ATT TCA GAA CAT TGT GCT GTC TGT  
 3721  
 CAG CAT ATG TAT ATC AGC TAC AAA ATA TAT TCA ACT TTG ACT TCT TTT GAC AAA GGA CTT  
 3751  
 TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT  
 3781  
 GTG ACC TTG ACT GAT AAT AAA TAT GTA ATA AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA  
 4021  
 AAC TCG

Ref 1.1

Sequence of BAC19 using primer HC5S11, which spans  
 nucleotides 3-22 of the cDNA. Exon sequence is underlined  
 and represents nucleotides 32-57.

CTCTCTGTCTTCATATCTTCAGGTTATAAAGNATTATTTACTAAAAGAANATTTCANGC  
 TATTTTCATTTAACTAGCTCAGTTTAAATCATGTATTTCCCTATAAAGGTTAGTCTTATTAAT  
 TTGACAAAACAATCAAACAATTCAAACCAGATCAAGTATGCTACCCCTGAAGTTACACC  
 ACTAGTTAAGAAATTAACAATCTAAATAATTGGTTTCTCCCCAGGCTCAAGGCTCCCTGA  
 TCAAGCTTAAGTAAAGCCAAGATCCAAATTAAGCCCTATGAAATTTAGAAACTCATAGAA  
 AAGTTTAAATTTTCTTTCTGACATTAACCAATTGTTATATTAIGCAAATAGAGGATT  
 NCAATTAATAAATTTTGAACCTGTTTACCAAGTTTTTTTGCAGCAAGNCTCTAAGAGCTT  
 AACTGGTCATGCATTGAATGCCGAGAGCAAAGAGGAATGGAGAGGGGNTGTAAGNSG  
 TTCCAATNTTACTGGAACCCACCACTATCTTTNGAAGTCTTGATACTTAACTGNGTGTA  
 RNTCTTTTAAAGCTNTANTAANTAAGAATCTATATGATTCGTTCTCTCNGCAAGNAG  
 TGCCTATGAAA

Sequence of BAC19 using primer HC5A310b, which spans nucleotides 557-580 of Exon sequence is underlined and represents nucleotides 510-553.

2013.11.11

Sequence of PAC11 using primer 3583, which spans nucleotides 106-1116 of the cDNA. Exon sequence is underlined and represents nucleotides 1110-1126.

Ref 4.2

Sequence of PAC13 using primer C8S7, which spans nucleotides 1156-2206 of the cDNA. . Exon sequence is underlined and represents nucleotides 2226-2731.

A T A A A A C T A A C C A G A N T A T T T A A A G C C C A A C A A N C T T T T T T T A A G A A T A G C A A N G  
A A C T A A A A G G G T T A T T T C A A A G A A C T T A A A T G C A G N C A A A C N A C T C C C C C A A G  
A S N G C A A C T A C T A A T G G G C A N A T C I N A A A G A A A T A T A G N C A A A G G N N N G G A A T C A  
T A A T A B B A G O N A C T A C T T A N G A A G C A C C A A C T G G G G A C C T G B A A C T G N A T N A G G N C C  
T C I A C A T A C A T C A T N N N A T A N C A T C C T G C A A C G A C C C C T G G A A G G A N A G A N G G N A  
T T C C T A N N K T A G A C A N G A G A N A A C T G G G G A C A T G C G A A G A G G N A A G C G A A G G G T T C A  
A G S S B A N G N A A C C A G C A G A N N C C A G G G N D C A N A C T N G N G G G G N N T G G G G G G N T X  
C T E N N C C C T A C H C C T N G N A N G A A C A G N G N N S T T G A N N T G G C T T T N G A N T A

CCANNAGATTNTTGNAACGNNGGTAGGCTTCTTTGTAGATTTATTGAAAATGTTTCGT  
ACTTCTACAAGTTTGCCCTGCTTCCFATAAAGAGTGAAANTCANTTTGAATCGACTGG  
TGGATAATTNTTCCATTTTTCTCAGGCAATTTNGAGTTACTCCAATAAATTCAAATAT  
GSSCCAGAGGAAATCATCTTTCAGATGGGCAGTGATTGGCCAGTCAGCAGGAGAAGC  
TGCTTATGCCTTGTTTGGTACATTGTGGAAAAACACACTTTAATAAATACGCANTCATG  
CTTGAGTACCCATCCTCCATCCCGCCACCCCCCAGTATGGCAAAAATCTGGTCAGAGT  
CCATTTGGGAATAATTCCATGGTTCCCGGGATCCCCAAAGCTTCCAGAAGTGCTGGCTG  
ATCAANGGAGTGTACAGTCAGTCCTGGGTGGCAAAAATGTCCCATTTTTTAAGTACCA  
AGCAAAGGTTCTTCTTNCAAGGGTTNCTAGGGCC

HC2A	-----
KIAA	ASGNLDKNARFSAIYRIDSNNKLSNDDMLKLLACFFKKPEKNAKLFPVILGNLDDITIDNVSSO
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----VLHHHQNPFFYDEIK
KIAA	KSFARKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVETRSFAFAAVLHHHQNPFFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	IELPTQLHEKHHLLLTFFHVSCDNSSFGSTKRDVVETQVGYSWLPLLDGRVVTSEQHI
KIAA	IELPTQLHEKHHLLLTFFHVSCDNSSFGSTKRDVVETQVGYSWLPLLDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	PVSANLPSGYLGYQELGMGRHYGPEIFWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIFWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGFARSTVSISLISNDARV
HC5	-----

HC2A	PTETSAALNRIYNYIYKLIHANEHETMIAPLITLINLEPVLT-PATREVAIVNTBV
KIAA	PTETSAALNRIYNYIYKLIHANEHETMIAPLITLINLEPVLT-PATREVAIVNTBV
rat	-----
HC4	-----MEIQVLIFFLSVILMQLFWVLPNMIHEDDVPISCPWV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NKCPALNENHLLPTETSAALNRIYNYIYKLIHANEHETMIAPLITLINLEPVLT-PATREVAIVNTBV
HC5	-----

FIG. 4B (1 of 5)

HC2A ITHVVAICHEEGLESHLRVYHYAVKAEPVASEYKT/HEELTKSMITILKPSADFLTSTN  
 KIAA ITHVVAQCHEEGLESHLRVYHYAVKAEPVASEYKT/HEELTKSMITILKPSADFLTSTN  
 rat -----  
 HC4 LPHIVSKCHEEGLESCYLSPFINKYSPFGKPSAPQAPLIHETLACMIALLYQSADFLAIN  
 HC1 LPHIVAKCHEEGLESHVQSYIKFVFKTR---ACKERP/HEDLAHNVITGLLK-SNDSPTVK  
 HC3 TQAMDPNCPMSSHTETSSPLQTLTGRLP---TKKL/HEELALQWVVCISG--SVR---E  
 HC5 -----

Cadherin  
 Cleavage

HC2A KLLKYSWFFFDVLIEMQAQHLIENSKVKLEENQRFPAVYHHAETVNNMLMPHITQKFGD  
 KIAA KLLKYSWFFFDVLIEMQAQHLIENSKVKLEENQRFPAVYHHAETVNNMLMPHITQKFRD  
 rat -----  
 HC4 KLLKYSWFFFEIIAKSMATYLLLEENKIKLTGQRFPPKAYHHAHSLFLAIC-IYHSQYAE  
 HC1 KVLHHSWFFFAIILFMAQHLIDTNKIQLFPPQRFPEVQNELDNLMVVLSDHVIWKVKD  
 HC3 SALQDAWFFFEELM/RSNVHHLVFNDKLEAEKSKSPFERFMDDAALVSTIASDVSRRQK  
 HC5 -----

HC2A NPEASNNANHS�AVEIHCFTFMDISEVFKQIN---NYIS--GFAPGDHKLDFEYKFEEL  
 KIAA NPEASNNANHS�AVEIHCFTFMDISEVFKQIN---NYIS--GFAPGDHKLDFEYKFEEL  
 rat -----  
 HC4 IPKESRMVNYSLASFLICCLTLMDESEVFKININ---DALS--GESPDPAVLAKYKFEEL  
 HC1 ALEETRIATHSVARFHLRCFTFMDISEVFKMNVN---NALS--MFSSGDLITLCQYFDFEL  
 HC3 DTEMVEILNNTSLAFFLMDLISVMDEGFVFETIKSCYHQVSSKLYSLNPVILVLELDFEL  
 HC5 -----

HC2A RVVCNHHHYIPLNLEM-----PEGFGRIQE-----VQDLQL----DYRLTDEF  
 KIAA RVVCNHHHYIPLNLEM-----PEGFGRIQE-----VQDLQL----DYRLTDEF  
 rat -----  
 HC4 QTICNHHHYIPLNLEM-----AFAPFKLQK-----VQDSNL----EYGLSDEY  
 HC1 QEVCOHLHFIPLCLPIF SANIPDPLTPSES-----TQELHASMPEYVITNEF  
 HC3 RIICSHLHYVTNLNPLCLLTPPASESPSVSSATISQSSGFSTNVQDQFIANMFEL--VPF  
 HC5 -----KPADTAPTSPGPSIS---SQNS--SCSSFGDQFIASMFDTISRVPA

1.1

Cadherin  
 EC motif

HC2A CRNHFLVGLLLREVGTAHQEFFE---VRLIAISVLKILLIKHSFDDRYASRSHQARIAT  
 KIAA CRNHFLVGLLLREVGTAHQEFFE---VRLIAISVLKILLIKHSFDDRYASRSHQARIAT  
 rat -----  
 HC4 CKHHFLVGLLLRETSIALQDNYE---IRYTAISVIKILLIKHAFDTRYQENQQAQIAQ  
 HC1 QPKHFIKGLLLREVGFIHQENQD---VRHIALAVLKILLIKHAFDTRYQEPKQAQIAC  
 HC3 EIDHYIAGNVLTELAIVLEIDAEGLFGIHKFVILNIFENLLSHHSDPRYSDPQIARVAM  
 HC5 SSTG-SFGNLFTELAASLFAVHGLPEVQPPAVVAIHLILSHHLLDFECVPEKVKIAA

HC2A IYLIIFNLIENVAQINIKRIVPFFVWAG-MTVKIESIALPAVNPLVTPQKGSTLDNLH  
 KIAA IYLIIFNLIENVAQINIKRIVPFFVWAG-MTVKIESIALPAVNPLVTPQKGSTLDNLH  
 rat -----  
 HC4 IYLIIFNGLLENIQFLAKRTIYSCAAMPNSASRDEFPQG-----FTSP--AN--PGSLIS  
 HC1 LYPLFYGMILENMPRIYLEDIYPTVNTSNIGSRDDLSTNGGFGSQTAIFHANSVDTSFS  
 HC3 IYLIIFNIMETWQIYFETETINQGHPICIATIIYEEF-----GQ---SMIS  
 HC5 IYLIIFNGLIILALICLITFTVATETVYF---TSQVIRELE-----GA---GLIT

Refs

HC2A K1AA rat HC4 HC1 HC3 HC5  
 KLLGALSGIASPYYTTSTENINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDHCQSS  
 KLLGALSGIASPYYTTSTENINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDHCQSS  
 -----  
 TRKPTANGSPONG-----HGIYREDSSIGSLIP-EGATGFPDQNGTGEN-----TRQS  
 KDWLNBIAPFSS-----IAISTYNHADSRASLASLDSNPFSTNERSSEKTDNCFKIPRPL  
 QTVAMAIAGTSVPQ-----LTPRGI FLLTSTSGRQHT-----  
 QNVAMAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----

2.1

HC2A K1AA rat HC4 HC1 HC3 HC5  
 TLGNVWRCDKLDQSEIKSLIMCFLYILKMSDDALFTYWN-KASTSEIMDFEFTISEVCL  
 TLGNVWRCDKLDQSEIKSLIMCFLYILKMSDDALFTYWN-KASTSEIMDFEFTISEVCL  
 -----  
 STRSVSQYNRLDQYEIPLSLIMCFLYIVHMISEDTLTYWN-FVSPQELINILILLEVCL  
 ALIGSTLRFDRLIQAETRESLLMCFLEHMTISYETLIAYWQ-FAPSPFVNDFFSIIIVCL  
 -----TFI AESSSESILICLLWVLENN-ADETVLQFWPTILSVLQINRLDOLLVCL  
 -----MLNADTFNLMICFLWINKL-ADQSLIRFWIADLPSTQINRILDLLFICV

HC2A K1AA rat HC4 HC1 HC3 HC5  
 HQFYNGKXYIAENQEGIG--PIVHDEHS-----CTLPVSRNRFGMH  
 HQFYNGKXYIAE-----FGH  
 -----  
 FEFYNGKXNIAEVHDAWLSKHFEGIDRES-----CTMPALRNEGVV  
 QNFRKLGKXNIIIFKIAAAF--FEVQSTQNGTLKGSNPSQTSGLIACWHPSTRREGH  
 SCFEYEGKXVFEEHNSLTFK--KSKDMKAF-----LEBAIGSIGAFQEMV  
 LCFEYEGKQSSDI VSTQVLQ--KSRDVHAF-----LEBAILRGEGAFGEH

HC2A K1AA rat HC4 HC1 HC3 HC5  
 HARLQQL-----GLDENS-----LTPNHSYCHSDADVLHQSLLEANIATEV  
 HARLQQL-----GLDENS-----LTPNHSYCHSDADVLHQSLLEANIATEV  
 -----  
 QARLQQL-----SLLESS-----FTLNHSSITTEADIHQALLLEGNTATEV  
 QHRSQTLPIIRG---NALSNNKL---LQMLDNTMTSINSNEIDI VHHVDTEANIAEG  
 RRSRGQIERSPSGSAFGSQENLRWRKDNTHWRQNTKLEKRAEIEHEALIDGNLATEAN  
 RRRAPGNDREFP-----GLENLRWRKQCTHWRQANEKLIETKAELOQEALISGNLATEAN

HC2A K1AA rat HC4 HC1 HC3 HC5  
 LTALDTLSLFTLAFKQILLADHGHNPLMKHVFEDVYLQFIQKHQSETALHNVFTALESLIF  
 LTALDTLSLFTLAFKQILLADHGHNPLMKHVFEDVYLQFIQKHQSETALHNVFTALESLIF  
 -----KLSRGHSPLMKHVFEDVYLQFIQKHQSEMALEHNVFTALESLIF  
 LTVLDTISFFTQC FKTHFLNNDGHNPLMKHVFEDIHLAFIENGQSEVSLFHVFALEAFIL  
 LTILDLVSLFTQI HQRQI QCCDCQNSLMKFGFDTYMLFFQVNSATALKHVFASLRLEW  
 LILNTERTVQTVG--LTER--FESLIGTULEVLEHGRACNQSAVYLQCHQFATORAL  
 LILNMLNIIAPF--ALP--KPEILVHVRVUNGNINLQWETTYLTHFEFTLEAL

3.1

HC2A K1AA rat HC4 HC1 HC3 HC5  
 FFFETFEFRAINAAAL YELLP TCHHLCIRTEACTLLVEFLMKNFL TEPHSEFVH  
 FFFETFEFRAINAAAL YELLP TCHHLCIRTEACTLLVEFLMKNFL TEPHSEFVH  
 -----  
 FFFETFEFRAINAAAL YELLP TCHHLCIRTEACTLLVEFLMKNFL TEPHSEFVH  
 FFFETFEFRAINAAAL YELLP TCHHLCIRTEACTLLVEFLMKNFL TEPHSEFVH  
 -----  
 FFFETFEFRAINAAAL YELLP TCHHLCIRTEACTLLVEFLMKNFL TEPHSEFVH  
 FFFETFEFRAINAAAL YELLP TCHHLCIRTEACTLLVEFLMKNFL TEPHSEFVH  
 -----

FIG. 4B (3 of 5)



HC2A ATAQMKREHENDPEMLVLDLQSLAKSYASTPELRRTWLDSMARIHVNGDLS EAAMCYVHV  
 KIAA ATAQMKREHENDPEMLVLDLQSLAKSYASTPELRRTWLDSMARIHVNGDLS EAAMCYVHV  
 rat ATAQMKREHENDPEMLVLDLQSLAKSYASTPELRRTWLDSMARIHVNGDLS EAAMCYVHV  
 HC4 ATAQMKREHENDPEMLVLDLQSLAKSYASTPELRRTWLDSMARIHVNGDLS EAAMCYVHV  
 HC1 ATAQMKREHENDPEMLVLDLQSLAKSYASTPELRRTWLDSMARIHVNGDLS EAAMCYVHV  
 HC3 ITVNMREHQEDPEMLVLDLQSLAKSYASTPELRRTWLDSMARIHVNGDLS EAAMCYVHV  
 HC5 ITVNMREHQEDPEMLVLDLQSLAKSYASTPELRRTWLDSMARIHVNGDLS EAAMCYVHV

## CH3

HC2A TALVAEYLTFRGV-----FLQGCYAFKMITPN  
 KIAA TALVAEYLTFRGV-----FLQGCYAFKMITPN  
 rat TALVAEYLTFRGV-----FLQGCYAFKMITPN  
 HC4 TALVAEYLTFRGV-----FLQGCYAFKMITPN  
 HC1 AALVAEYLTFRGV-----FLQGCYAFKMITPN  
 HC3 AALVAEYLTFRGV-----FLQGCYAFKMITPN  
 HC5 AALVAEYLTFRGV-----FLQGCYAFKMITPN

## ITAM

HC2A IDEEASIMHIVGMQD-----VHFNHIVIMELLEQCADGLWFAEFYELIADIYELI  
 KIAA IDEEASIMHIVGMQD-----VHFNHIVIMELLEQCADGLWFAEFYELIADIYELI  
 rat IDEEASIMHIVGMQD-----VHFNHIVIMELLEQCADGLWFAEFYELIADIYELI  
 HC4 IDEEASIMHIVGMQD-----VHFNHIVIMELLEQCADGLWFAEFYELIADIYELI  
 HC1 IDEEASIMHIVGMQD-----VHFNHIVIMELLEQCADGLWFAEFYELIADIYELI  
 HC3 IDEEASIMHIVGMQD-----VHFNHIVIMELLEQCADGLWFAEFYELIADIYELI  
 HC5 IDEEASIMHIVGMQD-----VHFNHIVIMELLEQCADGLWFAEFYELIADIYELI

HC2A EKKRDEFLARLYDTLHPAYSYVTEVMHCGERLLTYFERVAFFGQAAGQCFTEHTDWE  
 KIAA EKKRDEFLARLYDTLHPAYSYVTEVMHCGERLLTYFERVAFFGQAAGQCFTEHTDWE  
 rat EKKRDEFLARLYDTLHPAYSYVTEVMHCGERLLTYFERVAFFGQAAGQCFTEHTDWE  
 HC4 EKKRDEFLARLYDTLHPAYSYVTEVMHCGERLLTYFERVAFFGQAAGQCFTEHTDWE  
 HC1 EKKRDEFLARLYDTLHPAYSYVTEVMHCGERLLTYFERVAFFGQAAGQCFTEHTDWE  
 HC3 EKKRDEFLARLYDTLHPAYSYVTEVMHCGERLLTYFERVAFFGQAAGQCFTEHTDWE  
 HC5 EKKRDEFLARLYDTLHPAYSYVTEVMHCGERLLTYFERVAFFGQAAGQCFTEHTDWE

HC2A -FFEDDGGHLYHEPKLTPLSEISQRLILLSDDFGGSENVKNIQDSGHTNPHDLOSFA  
 KIAA -FFEDDGGHLYHEPKLTPLSEISQRLILLSDDFGGSENVKNIQDSGHTNPHDLOSFA  
 rat -FFEDDGGHLYHEPKLTPLSEISQRLILLSDDFGGSENVKNIQDSGHTNPHDLOSFA  
 HC4 -FFEDDGGHLYHEPKLTPLSEISQRLILLSDDFGGSENVKNIQDSGHTNPHDLOSFA  
 HC1 -FFEDDGGHLYHEPKLTPLSEISQRLILLSDDFGGSENVKNIQDSGHTNPHDLOSFA  
 HC3 -FFEDDGGHLYHEPKLTPLSEISQRLILLSDDFGGSENVKNIQDSGHTNPHDLOSFA  
 HC5 -FFEDDGGHLYHEPKLTPLSEISQRLILLSDDFGGSENVKNIQDSGHTNPHDLOSFA

## ITAM

HC2A YIQVTVTPPFEEKEIEDRKIDFEMHNINNFVFPETPTLSGKKHGGVAFQCKKRTILT  
 KIAA YIQVTVTPPFEEKEIEDRKIDFEMHNINNFVFPETPTLSGKKHGGVAFQCKKRTILT  
 rat YIQVTVTPPFEEKEIEDRKIDFEMHNINNFVFPETPTLSGKKHGGVAFQCKKRTILT  
 HC4 YIQVTVTPPFEEKEIEDRKIDFEMHNINNFVFPETPTLSGKKHGGVAFQCKKRTILT  
 HC1 YIQVTVTPPFEEKEIEDRKIDFEMHNINNFVFPETPTLSGKKHGGVAFQCKKRTILT  
 HC3 YIQVTVTPPFEEKEIEDRKIDFEMHNINNFVFPETPTLSGKKHGGVAFQCKKRTILT  
 HC5 YIQVTVTPPFEEKEIEDRKIDFEMHNINNFVFPETPTLSGKKHGGVAFQCKKRTILT

Coiled-Coil 1

HC2A	IHCFFPYTKRRI FVMYQHHTLNNPIEVAIDEMSHFVAELRQLQSSAEVDMIHQLQLF LQG SV
KIAA	IHCFFPYTKRRI FVMYQHHTLNNPIEVAIDEMSHFVAELRQLQSSAEVDMIHQLQLF LQG SV
rat	IHCFFPYTKRRI FVMYQHHTLNNPIEVAIDEMSHFVAELRQLQSSAEVDMIHQLQLF LQG SV
HC4	SNSEPPYVFRRI PINCEQQINLKPIDGATDEIIFKTAELQKLCSSFDVDMIQQLQLF LQGVV
HC1	HLFFPYVFRIQVLSQSSTRNNPIEVAIDEMSHFVSELNQLCTNEEVDMISLQLQLF LQGVV
HC3	HAFFPYITFVNVVTHKEEITLTRI EVAIEDMKRRTQELAFATHQDPADPKMLQMV LQGVV
HC5	MHAFFPYITFELSVQKEEPVLTTRI EVAIEDMKRRTIQLAVAINQEPDPAKMLQMV LQGVV

Coiled-Coil 1

HC2A	VMQVNAGILAYAHAFLLDDTNTKRYPDNKVKLIIEVFRQFVEACGQALAVNERLIEEDQHE
KIAA	VMQVNAGILAYAHAFLLDDTNTKRYPDNKVKLIIEVFRQFVEACGQALAVNERLIEEDQHE
rat	VMQVNAGILAYAHAFLLDDTNTKRYPDNKVKLIIEVFRQFVEACGQALAVNERLIEEDQHE
HC4	VMQVNAGILAYAHAFLLDSSQASHYPPKKVSELI DMELFIQACSLALEINERLIEEDQHE
HC1	VMQVNAGILAYAHAFLEETNAKRYPDNQVKLIIEIIFQFADACGQALAVNERLIEEDQHE
HC3	ITTVNQGLEVAQVFLSEIPSDILFRHHNKILLCFLDFTKRCEDALEHNSLIGPVQHE
HC5	CATVNQGLEVAQVFLAEIPADIKLYRHHNKILLCFLDFIMRCGEAVHNSRLITAIQHE

Coiled-Coil 2

HC2A	IQEEMFANYFIMAHELSEIMHEKICPLEKKTSLVLENLHIFNAISGTPTS TIVHGNTSS
KIAA	IQEEMFANYFIMAHELSEIMHEKLG-----
rat	IQEEMFANYFIRKHELSDIIVFRICPGEDKRATKFIASHLQRHQEDTNEHSCSRVDPHLS
HC4	IQEGLFSNFRDMVHELSDIIEKILQEDTMHSPWMSNTLHVFCALSGTSLRGYGSIRLA
HC1	IQEELFSHYKMDLSELSTVMNEKITGRDDLKSK---FGVDQCTCTEVISFATPALPTVSS
HC3	IQRELG----KLSS-----P-----
HC5	IQEELFKYNKLNKENLRPMIERKIPELYKPIFRVESQARDSFHRSSFLCETQLSQGS--

IBM

HC2A	LSVV-----
KIAA	-----
rat	CVTLPHPEPHVGTCTFVMCKLRTTFRANHWFCQAQEEANGNGREKEPWTIVFNSRFYRSWCK
HC4	EV-----
HC1	SAEV-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	-----
rat	CHFF
HC4	-----
HC1	-----
HC3	-----
HC5	-----
ENTVLT	-----

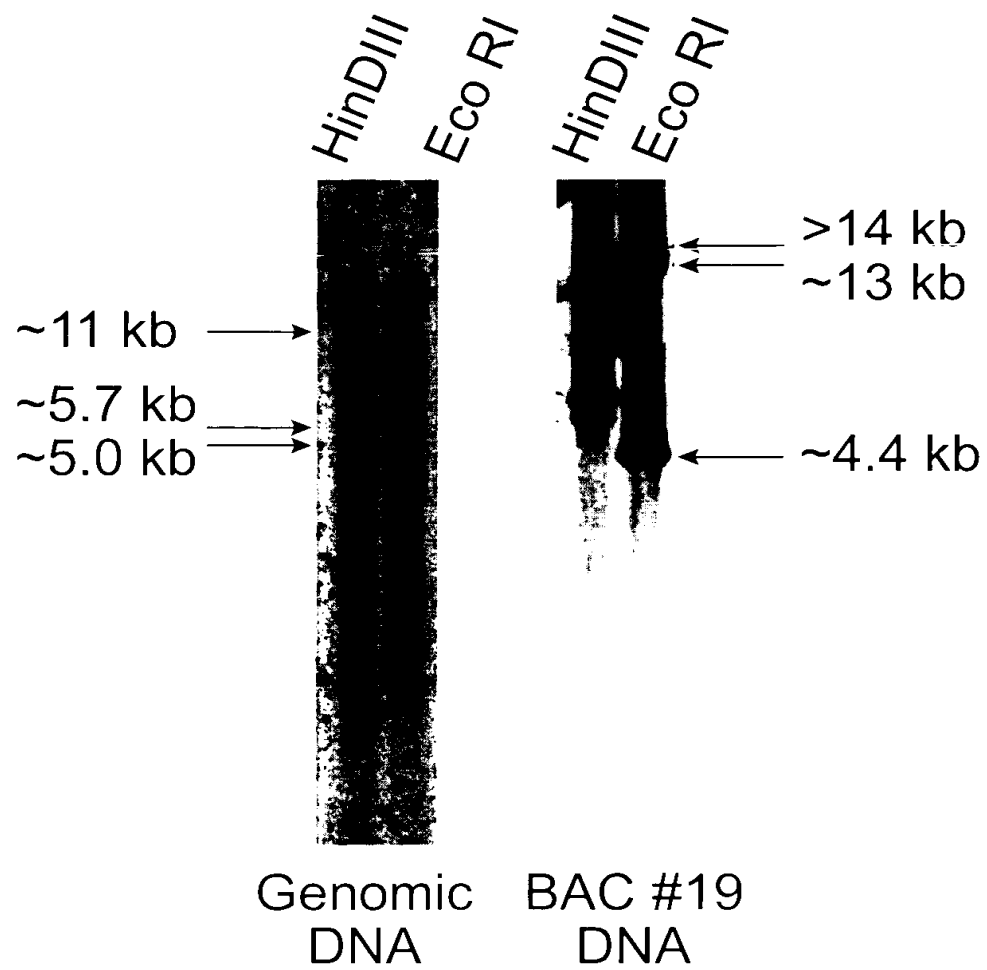


FIG. 5

-1111

CGGTAACCGCCATTTTGTCTCCCTGTAACAATTTACGGCGCCGTGTAAGTGTGAATCTTTCAAGCCCTCAGTTTTATGACC  
CTGTGAGAGAGTGGAGTTTCAAGGAGTTTGTG -1

1/1	31/11
ATG ACA CAG CTG AAC AGC CTG GAT GTG CAG CTT GGC CAG GAG CTC GGG GAC TTC ACT GAT	
Met Thr His Leu Asn Ser Leu Asp Val Ala Leu Ala Gln Glu Leu Gly Asp Phe Thr Asp	
41/41	81/81
GAC GAC TTG GAC GTG GTG TTC ACG CCA AAG GAA TGT AGG ACT TTG CAG CCC TGT TTG CCG	
asp asp leu asp val val phe thr pro lys glu cys arg thr leu gln pro ser leu pro	
121/41	151/51
GAG GAA GGG GTT GAA CTG GAC CCT CAT GTC AGG GAC TGT GTT CAG ACC TAC ATC CGT GAG	
glu glu gly val glu leu asp pro his val arg asp cys val gln thr tyr ile arg glu	
181/61	211/71
TGG CTA ATC CTG AAC CGG AAA AAC CAA GGA AGT CCA GAA ATC TGT GGC TTT AAA AAG ACT	
trp leu ile val asn arg lys asn gln gly ser pro glu ile cys gly phe lys lys thr	
241/81	271/91
GGA TGT CGA AAA GAT TTT CAC AAG ACG CTT CCG AAA CAG ACG TTT GAG TCS GAA ACC TTG	
gly ser arg lys asp phe his lys thr leu pro lys gln thr phe glu ser glu thr leu	
301/101	331/111
GAG TGC AGT GAA CCC GCT GCT CAG GCA GGC CCC CGC CAC TTA AAC GTG CTG TGC GAC GTG	
glu cys ser glu pro ala ala gln ala gly pro arg his leu asn val leu cys asp val	
361/121	391/131
TGT GGG AAA GGC CCC GTC ACT GCC TGT GAC TTT GAC CTC CGC AGC CTG CAG CCT GAC AAG	
ser gly lys gly pro val thr ala cys asp phe asp leu arg ser leu gln pro asp lys	
421/141	451/151
CGG CTA GAA AAC CTC CTG CAG CAA GTG AGT GCC GAG GAC TTT GAG AAG CAG AAC GAG GAG	
arg leu glu asn leu leu gln gln val ser ala glu asp phe glu lys gln asn glu glu	
481/161	511/171
GCC CGG AGG ACC AAC AGG CAG GCC GAG CTC TTT GCC CTT TAC CCA TCA GTG GAC GAG GAG	
ala arg arg thr asn arg gln ala glu leu phe ala leu tyr pro ser val asp glu glu	
541/181	571/191
GAT GCT GTG GAA ATA CGT CCA GTA CCA GAA TGT CCC AAG GAA CAC CTG GGC AAC AGA ATA	
asp ala val glu ile arg pro val pro glu cys pro lys glu his leu gly asn arg ile	
601/201	631/211
TTG GTC AAG TTG CTG ACC TTG AAG TTC GAG ATT GAA ATT GAG CCC CTG TTT GGC AGC ATT	
leu val lys leu leu thr leu lys phe glu ile glu ile glu pro leu phe ala ser ile	
661/221	691/231
CCC CTC TAC GAT GTT AAA CAA ACG AAA AAG ATC TCA GAA AAT TTT CAC TGT GAC CTG AAC	
ala leu tyr asp val lys glu arg lys lys ile ser glu asn phe his cys asp leu asn	
721/241	751/251
TCT CAT CAG TTT AAA GGA TTT TTT CCA GGT CAC ACC CTT TTA CTG GGT GAA TGA AGT CAG	
ser thr thr phe lys gly phe leu arg ala his thr pro ser val ala ala ser ser ala	
781/261	811/271
GTA GAA TTA GAA GAT TTT TTA GAT AAT TAT TTA GAT TTA GAT TTA GAT TTA GAT TTA GAT	
ala ala ser ala val phe ser val thr tyr pro ser ser asp ile tyr leu val val lys	
841/281	871/291
ATT GAA AAA ATC CTC CAG CAG GGA GAT ATT GGA GAC TGT GCA GAG CCC TAC ACG GTT ATC	
ile glu lys val leu asn gln gly asp ile cly asp cys ala glu pro tyr thr val ile	
901/301	931/311
AAA GAA AAT GAT GGT GGA AAG ACT AAA GAA AAG ATT GAA AAA CTA AAA CTC CTA GGT GAA	
lys ala ser asp gly gly lys ser lys ala lys ala gln lys leu lys leu gln ala ala	
961/321	991/331
GAT TTA TTA GAT GAT TTA TTA TTA TTA TTA TTA TTA TTA TTA TTA TTA TTA TTA TTA	
asp thr thr asp asp thr thr thr thr thr thr thr thr thr thr thr thr thr thr thr	

FIG. 6A (1 of 6)



2161/721  
 GTG GTC TTC CTG CAC CTG CTG CTG GAG AAG CTC TTC CAG CTG TCC GTG CAG CCC ATG GTC  
 val leu phe leu his leu val leu asp lys leu phe gln leu ser val gln pro met val  
 2281/761  
 ATC GCT GGC CAG ACA GCC AAC TTC TCC CAG TTT GCC TTC GAG TCC GTG GTS GCC ATC GCC  
 ile ala gly gln thr ala asn phe ser gln phe ala phe glu ser val val ala ile ala  
 2281/761  
 AAC AGT CTG CAC AAC AGC AAG GAC CTG AGC AAG GAC CAG CAT GGG AGG AAC TCC CTG CTG  
 asn ser leu his asn ser lys asp leu ser lys asp gln his gly arg asn cys leu leu  
 2341/781  
 GCT TCC TAC CTG CAC TAC CTC TTC CCC CTG CCA GAG GTG CAA AGG GAT GTG CCC AAG TCA  
 ala ser tyr val his tyr val phe arg leu pro glu val gln arg asp val pro lys ser  
 2401/801  
 GCG GCT CCC ACT GCC CTC CTA GAC CTT CGG AGC TAC CAC ACC TAT GGC CGC ACA TCA GGT  
 gly ala pro thr ala leu leu asp pro arg ser tyr his thr tyr gly arg thr ser ala  
 2461/821  
 GCT GCT GTG AGT TCA AAG CTG CTG CAG CCC CCG CTG ATG AGC AGC AGT AAC CCA GAC CTC  
 ala ala val ser ser lys leu leu gln ala arg val met ser ser ser asn pro asp leu  
 2521/841  
 GCG GGC ACA CAC TCC GCA GCA GAC GAG GAA CTG AAG AAC ATC ATG TCT TCA AAG ATC GCC  
 ala gly thr his ser ala ala asp glu glu val lys asn ile met ser ser lys ile ala  
 2581/861  
 GAT CGC AAC TGC AGC CGA ATG TCT TAC TAT TGC TCT GGC AGT AGT GAT GCT CCA AGT TCA  
 asp arg asn cys ser arg met ser tyr tyr cys ser gly ser ser asp ala pro ser ser  
 2641/881  
 CCT GCA GCC CCA AGG CCA GCC AGC AAA AAG CAT TTC CAT GAG GAG CTT GCC CTT CAG ATG  
 pro ala ala pro arg pro ala ser lys lys his phe his glu glu leu ala leu gln met  
 2701/901  
 GTG GTC AGC ACC GGA ATG GTG AAA AGC ATG GCG CAG CAC GTA CAT AAC ATG GAC AAA CGG  
 val val ser thr gly met val lys ser met ala gln his val his asn met asp lys arg  
 2761/921  
 GAC AGT TTT CGG AGG ACT CGT TTT TCT GAC CTT TTC ATG GAT GAC ATA ACT ACT ATT GTT  
 asp ser phe arg arg thr arg phe ser asp arg phe met asp asp ile thr thr ile val  
 2821/941  
 AAT GTG GTC ACC TCG GAA ATT GCA GCC CTT TTA GTA AAA CCA CAG AAG GAA AAT GAA CAG  
 asn val val thr ser glu ile ala ala leu leu val lys pro gln lys glu asn glu gln  
 2881/961  
 GCG GAA AAG ATG AAC ATC AGC CTG GCT TTC TTC TTG TAT GAC CTT CTC CCC CTC ATG GAT  
 ala glu lys met asn ile ser leu ala phe phe leu tyr asp leu leu ser leu met asp  
 2941/981  
 GAG GAT TTC CTG TTT AAT CTC ATT ATA AAT CAT TAT TGT AAT CAG CTG TTA GTC AAT CTC ACT  
 arg gly phe val phe asn leu ile arg his tyr cys ser gln leu ser ala lys leu ser  
 3001/1001  
 AAT TTT TTA AAT TTC ATT TTT ATT AAT TTA GAG TTT CTG AAT ATT TTT TGT AAT CAT GAG  
 asn leu pro thr leu ile ser met arg leu leu phe leu arg ile leu cys ser his his  
 3061/1021  
 CAT TAC CTC AAT CTG AAG CTT TTT TTT ATG AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT  
 his tyr leu asn leu asn leu phe phe met asn ala asp thr ala pro thr ser pro cys  
 3121/1041  
 ATT TTT AAT TTT TTT TAA AAT TTA AAT TTT TGT TTT AAT TTT TAA GAG CAG AAT ATG GCT  
 pro ser ile ser ser gln asn leu ser ser thr ser ser phe ala asp gln lys ile ala  
 3181/1061

FIG. 6A (3 of 6)

3311/1101	3331/1111
GCT GTG AGT GGA ATT CAG AGC CTC CTA AGT	TAT CAG GAC CTG GAC CCA CGC TGT GTG AAA
ala val ser ala ile his ser leu leu ser	ser his asp leu asp pro arg cys val lys
3361/1111	3401/1121
GGA GAG GTG AAG CTC AAA ATC GCG GGT GTT	TAC CTA CTT TTA GTT GCG ATC ATT TTG GAT
pro gls val lys val lys ile ala ala leu	tyr leu pro leu val gly ile ile leu asp
3431/1141	3451/1151
GCT TTG CCA CAG CTC TGT GAC TTT ACA GTT	GGA GAT ACT CGC AGA TAC CGC ACC AGT GGC
ala leu pro gln leu cys asp phe thr val	ala asp thr arg arg tyr arg thr ser gly
3481/1161	3511/1171
TGG GAT GAA GAA CAA GAA GGA GCG GGT GGC	ATT AAC CAG AAT GTG GCT CTG GCG ATA GCA
ser asp glu glu gln glu gly ala gly ala	ile asn gln asn val ala leu ala ile ala
3541/1181	3571/1191
GGG AAT AAT TTC AAT TTG AAA ACA AGT GGA	ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG
gly asn asn phe asn leu lys thr ser gly	ile val leu ser ser leu pro tyr lys gln
3601/1201	3631/1211
TAC AAC ATC CTG AAC GCG GAC ACT ACT CGC	AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG
tyr asn met leu asn ala asp thr thr arg	asn leu met ile cys phe leu trp ile met
3661/1221	3691/1231
AAA AAT GCT GAT CAG AGC CTC ATT AGG AAG	TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC
lys asn ala asp gln ser leu ile arg lys	trp ile ala asp leu pro ser thr gln leu
3721/1241	3751/1251
AAC AGG ATT TTA GAT CTA CTT TTC ATC TGT	GCG CTA TGT TTT GAG TAT AAG GGA AAA CAG
asn arg ile leu asp leu leu phe ile cys	val leu cys phe glu tyr lys gly lys gln
3781/1261	3811/1271
AGT TCT GAC AAA GTC AGT ACC CAA GTC CTG	CAG AAG TCA AGG GAT GTC AAG GCG CGG CTG
ser ser asp lys val ser thr gln val leu	gln lys ser arg asp val lys ala arg leu
3841/1281	3871/1291
GAA GAG GCT TTG CTG CGT GCG GAA GGG GCG	AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA
glu glu ala leu leu arg gly glu gly ala	arg gly glu met met arg arg arg ala pro
3901/1301	3931/1311
GGG AAC GAC CGA TTT CCA GGC CTA AAT GAA	AAT TTG AGA TGG AAG AAA GAG TAG ACA CAT
gly asn asp arg phe pro gly leu asn glu	asn leu arg trp lys lys glu gln thr his
3961/1321	3991/1331
TGG CGG CAA GCT AAT GAG AAG CTA GAT AAA	ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG
trp arg gln ala asn glu lys leu asp lys	thr lys ala glu leu asp gln glu ala leu
4021/1341	4051/1351
ATC ACT GGC AAT CTG GCT ACA GAA GCA CAT	TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT
ile ser gly asn leu ala thr glu ala his	leu ile ile leu asp met gln glu asn ile
4081/1361	4111/1371
ATC CAG GCG AGC TCG GCT CTG GAC TGT AAA	GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG
ile ala ala ser ser ala leu asp cys lys	asp ser leu leu gly gly val leu arg val
4141/1381	4171/1391
TGG GTG AAT TTT GTT AAT TAT TAT CAG AAT	AAT AAT TAT TTT AAT TAT TTT TTT TTA ATA
trp val asp pro leu asp tyr arg ala ser	thr thr tyr leu thr thr cys phe ala thr
4201/1401	4231/1411
TTT GTT AAT TTT ATT TTT AAT TTT GAA GAT	TTA CTC TTT GAA GAG GAG GTG GAA CAG TGT
leu arg ala leu ile ala lys phe gly asp	leu leu phe glu glu glu val glu gln cys
4261/1421	4291/1431
TTT GAC CTA TGT CAC CAA GTC CTG CAT CAC	TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC
phe asp leu cys his gln val leu his his	cys ser ser ser met asp val thr arg ser
4321/1441	4351/1451
GAA GAT TTT GAT AAT TTT TAT TTT TTT ATG	AGG TTC AAT TTT GGA GGT ACC AGT AAT TTT
gln asp thr glu asp leu asp thr thr thr	arg thr thr thr thr thr thr thr thr thr

FIG. 6A (4 of 6)

4441/1481 4471/1491  
 TTT AAT GAA GAG CAG CTG AGA AGA TCG TTS AGG ACA ATT TTG GGC TAT TCA GAA GAG GAC  
 phe ala ala gln his leu arg arg ser leu arg thr ile leu ala tyr ser gln glu asp  
 4541/1501 4531/1511  
 ACA GGC ATG CAG ATG ACT CCT TTT CCG ACC CAG GTG GAG GAA CTT CTC TGT AAT CTS AAT  
 thr ala met gln met thr pro phe pro thr gln val glu glu leu leu cys asn leu asn  
 4561/1521 4591/1531  
 AGC ATC TTA TAT GAC ACA CTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG  
 ser ile leu tyr asp thr val lys met arg glu phe gln glu asp pro glu met leu met  
 4621/1541 4651/1551  
 GAT CTC ATG TAC AGA ATT GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTS ACC TGG  
 asp leu met tyr arg ile ala lys ser tyr gln ala ser pro asp leu arg leu thr trp  
 4681/1561 4711/1571  
 CTC CAG AAC ATG GCA GAG AAA CAG ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC  
 leu gln asn met ala glu lys his thr lys lys lys cys tyr thr glu ala ala met cys  
 4741/1581 4771/1591  
 CTG GTG CAC GCC GCT GCG TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC  
 leu val his ala ala ala leu val ala glu tyr leu ser met leu glu asp his ser tyr  
 4801/1601 4831/1611  
 CTG CCC GTG GGC AGT GTC AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG  
 leu pro val gly ser val ser phe gln asn ile ser ser asn val leu glu glu ser val  
 4861/1621 4891/1631  
 GTC TCT GAG GAC ACC CTG TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC  
 val ser glu asp thr leu ser pro asp glu asp gly val cys ala gly gln tyr phe thr  
 4921/1641 4951/1651  
 GAG AGT GGC CTG GTA GGC CTC CTG GAG CAG GGC GCG GAG CTC TTC AGC ACG GGA GGC TTA  
 glu ser gly leu val gly leu leu glu gln ala ala glu leu phe ser thr gly gly leu  
 4981/1661 5011/1671  
 TAT GAG ACA GTT AAT GAG GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA  
 tyr glu thr val asn glu val tyr lys leu val ile pro ile leu glu ala his arg glu  
 5041/1681 5071/1691  
 TTC CGG AAG CTG ACA CTC ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC  
 phe arg lys leu thr leu thr his ser lys leu gln arg ala phe asp ser ile val asn  
 5101/1701 5131/1711  
 AAG GAT CAT AAG AGA ATG TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT  
 lys asp his lys arg met phe gly thr tyr phe arg val gly phe phe gly ser lys phe  
 5161/1721 5191/1731  
 GGG GAT TTG GAT GAA CAG GAG ITT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG  
 gly asp leu asp glu gln glu phe val tyr lys glu pro ala ile thr lys leu pro glu  
 5221/1741 5251/1751  
 ATC TCA CAT AGA CTA GAG CGA TTT TAT GGT CTA TGT TTT GGT GCA GAA TTT CTA GAA CTC  
 ile ser thr arg ala leu gln ala phe tyr gly gln cys phe gly ala gln phe val gln val  
 5281/1761 5311/1771  
 ATT AAA GAT TTT AAT TTT TTT GAT AAA AAT AAG TTT GAT TTT AAT AAG CTT TAT ATA TAT  
 ile lys arg leu thr thr thr val arg lys thr thr thr leu arg phe ala tyr ile gln  
 5341/1781 5371/1791  
 ATC ACT TTT GTC GAG CCG TAC ITT GAT GAT TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT  
 ile thr phe val glu pro tyr phe asp glu tyr glu met lys asp arg val thr tyr phe  
 5401/1801 5431/1811  
 GAG AAG AAT TTC AAG CTC CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG  
 glu lys asn phe asn leu arg arg phe met tyr thr thr pr phe thr leu gln gly arg  
 5461/1821 5491/1831  
 CTT TTT GAA GAT TTT CAT GAG GAT TAT GAA GAT TAT GAA GAT TTT TTT AAT AAT ATT TTT GAT

FIG. 6A (5 of 6)



5561/1861	5611/1871
ATT GAA GTT GCT ATT GAA GAG ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC	
ile glu val ala ile glu asp met lys lys lys thr leu glu leu ala val ala ile asn	
5641/1881	5671/1891
CAG GAG CCG CCT GAT GCA AAG ATG CTT CAG ATG GTG CTG CAA GCG TCT GTG GGA GCT ACT	
glu glu pro pro asp ala lys met leu glu met val leu glu gly ser val gly ala thr	
5701/1901	5731/1911
GTA AAT CAG GGA CCA CTG GAA GTA GCG CAA GTG CTT TTG GCT GAA ATT CCT GCT GAT CCA	
val asn glu gly pro leu glu val ala glu val phe leu ala ala ile pro ala asp pro	
5761/1921	5791/1931
AAA CTC TAT CGA CAT CAC AAC AAG TTG AGS TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT	
lys leu tyr arg his his asn lys leu arg leu cys phe lys glu phe ile met arg cys	
5821/1941	5851/1951
GGT GAA GCT GTA GAG AAA AAC AAG CGT CTG ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG	
gly glu ala val glu lys asn lys arg leu ile thr ala asp glu arg glu tyr gln gln	
5881/1961	5911/1971
GAA CTC AAA AAG AAC TAT AAC AAG CTA AAA GAG AAC CTG AGG CCA ATG ATC GAG CGG AAA	
glu leu lys lys asn tyr asn lys leu lys glu asn leu arg pro met ile glu arg lys	
5941/1981	5971/1991
ATT CCA GAA CTG TAC AAG CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC	
ile pro glu leu tyr lys pro ile phe arg val glu ser glu lys arg asp ser phe his	
6001/2001	6031/2011
AGA TCT AGT TTC AGG AAA TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA	
arg ser ser phe arg lys cys glu thr glu leu ser glu gly ser OCH	

GAAAAGCCATCTTCATTCGTGGAGACTGTGGCCCTGCAACCCCTGAGAGAGGACTTGCTGGTACTTAAAAAATGGGACATT  
 TGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTCTGGAAGCTTTGGGATCCCAGGAACCATGGAATTATT  
 CCCCAAATGGACTCTGACCAGATTTTTGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGCATGAATGGGTAT  
 TTATTAAAGTGTGTTTTTCCACAATGTACCAACAAGGCATAAGCAGCTTCTCCTGCTGACTGGCCAAACACTGCCCATC  
 TGAGAGATGATTTCTCTGGCCCATATTTGAATTTATTGGAGTAACTCAAATTGCCTGAGGAAAAATGGAAAAATTATCC  
 ACCAGTCGATTCAAACCTGAATTTCACTCTTTATAGGAAGGCAGGGCAAACTTGTAGGAGTACGAAACATTTTCAATAAAAT  
 CTACAAAGGGGAAGCCTTACTACAATTCAAAAATCATCATGGTTGGAATTTGGGAGGAGATTATTGTTGAACCTTGTTAC  
 CCTTTGGTAATGGTGGACTAATGGCTGTATAGTTATTTTGGTTTTATTATTACGTTACATTAATTTAACATGCATTTA  
 TAGAAGAATACATTCAAAGCACTGATGTAGGAGATACAGGCTACTTGGAGCAGTCAGCCAAAAATCACAGATACTGCTTT  
 CACTTAAATGGAAACAATTCTCCGATAATGCTTTGCTTTTTTTCTTATGTACTCTTGTGTACTATCTATTTTTCTCCTC  
 TCTGGGACCAAGTTCTTTTTATAAGCAATAATATCTCTGTTTTCATTTGAGAACATTGTGCTGTCTGTACGATATGT  
 ATATCAGCTACAAAATATATTCAACTTTCACTTCTTTTACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTG  
 AGAATTAAATTATATATTTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAATTGCAAGCTAAAAAAA  
 AAAAAAAAAAACTCG

FIG. 6A (6 of 6)

A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-5 cDNA isoforms

Isoform	Nucleotide(s)	Consequence
1	1727	C to T change; mis-sense mutation changing codon from alanine to valine
2	1749	A to G change; silent mutation
3	2277	G to C change; silent mutation
4	2853	C to T change; silent mutation
5	3427	A to G change; mis-sense mutation changing codon from lysine to glutamic acid
6	3777	C to T change; silent mutation

B. Alternative splices

Isoform	Difference	Nucleotide(s)	Consequence
1	exon deletion	1806-1944	premature, in-frame stop codon leading to the production of a truncated, most likely soluble protein
2	exon insertion	between 2857 and 2858	additional, in-frame 48 nucleotide exon that contains a stop codon at the second codon, which would lead to a truncated, most likely soluble protein

These differences may be found separately or together in various combinations in the different human CLASP-5 isoforms

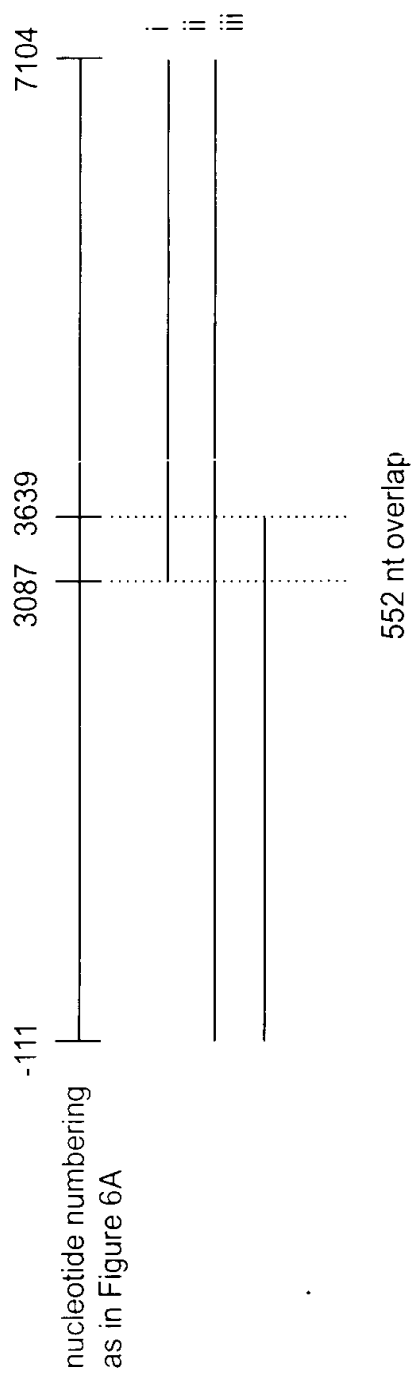


FIG. 6C

1st partial exon (nucleotides 3793 to 3952)

CCAGCTGTCAAGCAAGCTCAGTAACCTTCCAAAGCTCATTTCATGAGGCTAG  
AATTTCCTGAGAATCTCTCTAGCCATGAGTATTAAGCTCAATCTGAACCTTTT  
TTATGAATGCTGATACTGCTCAACATCTCTTGTCTTCCATATCTTCCAG  
GTAATAAAAGAAATTAATTAAGTAAAAGAATTATTCAGCTAT

2nd exon (nucleotides 5809 to 5944)

GCTCAIAAAATGGCTCTTACGTTTCTGTAGAACTCAAGCTCCTGCTCCAGCT  
TCCAGGACCAGAAAGATCGCCAGCATGTTCCGATCTGACTTCCGAGTACCGCCA  
GTAGCACTTCTCTCACTGGCTCTCTTTCAGAGAACTGGCTGCTGCCCTGGATG  
CCGAAAGGGAAGGCTATGTTTCTGGCATTTAAAATGGAAGATGAAGC

3rd exon (nucleotides 13662 to 13831)

CATAAGCTCTTGATTCCTGTGTGTGTGCCAACAAGTAATCAGCAAAGTACAAAGG  
AAAGCTGTCACTGTCAATTTCAGAGCTGTCTAAGTTCTCACGACCTGGACCCAC  
GCTGTCTCAAAACAGAGGTAAGGTCAAAATCGCCGCCCTTTACCTACCTTTA  
GTTGGCATCATTTTGGATCTTTTGGCACAGCTCTCTGACTTTACAGGTAATGG  
CCCTTCTGTCTTTCTTTCTTGGATTG

4th exon (nucleotides 16948 to 17087)

TGTTTACCTTGACATCACAAACGATGTTTTCAATTGCACTTGCAGATACTCGCA  
GATACCGCACACAGTGGCTCGGATGAAGAAACAAGAAGGAGCCGGTCCCATTA  
ACCAGAAATGTGGCTCTGGCCATAGCAGGGAATAATTTCAATTTGAAAACAAG  
TGGAATAGTGGCTGTCTTCTTGGTATGTTGGTGCACATGTGTCTGGTTGATTTT  
TCAT

5th exon (nucleotides 19281 to 19463)

TGCTCTCCATCCCCCAATCTGCTTCCCTTCAGCCCTATAAGCACTACAACATG  
CTGAAAGCGGACACTACTGGCAAGCTCATGATCTGCTTCTCTGGATCATGAA  
AAATGTGATCAGAGCTCATTAGGAATGGATTGCTGACCTGCCATCAACG  
CAGCTAACAGGATTTTACATCTACTTTTCATCTGTGTCTTATGTTTTGAGTAT  
AAGGTAAGTCTGGAAGTCACTATTATACAGC

6th exon (nucleotides 19829 to 19953)

CACCAAAGGACATGTCTCTTACCTCTCTCTTGTCCAGGGAACAAGATTCT  
GACAAAGTCACTACCCAAGTCTTGCAAGAGTCAAGGGATGTCAAGGCCCGG  
CTGGAAGAGCTTTTGGCTGGGTGGGGAAGGCGCCAGAGGGGAGATGATGCGC  
CGCCGGGCTCCAGGTGTGTTGGACTGGCCCTTCTGCTCTCTGTCAAGC



14th exon (nucleotides 38125 to 39268)

CTGTTCTCCAGGCTTATACCTGTGGTCTCTTCAAAATATTTCTTCCAAATGTGCT  
GGAGGAGTCTGTGGTCTCTCAGGACACCCCTGTACCTGACGAGGATGGGGTGTG  
CGCAAGCCAGTACTTCACCCAGAGTGGGCTGGTAGGGCTCCTGGAGCAGG  
CCGCGAGAGCTCTTCAGCACGGTCAAGTGCCAGAGGGGATCCCCGGGGCTGGC  
C

15th exon (nucleotides 40166 to 40197)

AATTCTCTCTGATGCTCTTCTCTCTTCCAAAGGAGGCTTATATGAGACAGT  
TAATGAGGTCTACAAGCTGGTCAATCCCATCCTAGAAGCGCATCGAGAAATTC  
CGGAAGCTGACACTCACTCACAACAAGCTGGCAGAGAGCCTTCGACAGCATCG  
TTAACAAGGTAGCCGGGAGCTTGGCTGGCAGGTCCTTGTTAC

16th exon (nucleotides 40755 to 40889)

TAAGGAGAGCTTTTTATATTTTGTTCCTCAGGATCATAAGAGAAATGTTTGGAA  
CTACTTCCGAGTTGGTITTCTTGGATCCAAATTTGGGGATTTGSATGAACAG  
GAGTTTGTCTACAAAGAGCCTGCAATTACCAAGCTTCCTGAGATCTCACATAG  
ACTAGAGGTAAGAAAATGATTTCTGTGCGCCTGACTTGGTACACTTTAC

17th exon (nucleotides 42307 to 42396)

AACCTTTATAAACTGTTGGTCTTCTTACCTAGCCATTTTATGGTCAATGTTTT  
GGTGCAGAAATTTGTGGAAGTGATTAAAGACTCCACTCCTGTGGACAAAACCA  
AGTTGGATCCTAACAAGGTATACAAAAATTTACAAAAACTAACCATCAAGC

18th exon (nucleotides 45250 to 45486)

CTTCTCCCTCCGTCCCTTTTCCCCCTTAGGGCTACATACAGATCACTTTTGTG  
GAGCCCTACCTTGATGAGTATGAGATGAAAGACAGGGTCACATACCTTGAGAAGA  
ATTICAACTCCGGAGGTTATGTATACCACCCCGTTCAACCTGAGAGGG  
GCGGCTCCGGGAGAGCTCCATGAGCAGTACAGAAGGAACACAGTCTCTGAC  
CACTATGTACGGCTTCCCTTACATCAAGACTAGGATCAGCGTCACTCCAGAAG  
GAGGAGCTAATCCACCCAAAGGATGGGCACCACTTGATGAGT

19th exon (nucleotides 48664 to 48697)

ACAGTGATTTCCCTATGTTTADGTTCTCATGTTCAAGTTTGTTTTGATACCGATTG  
AAGTTGCTAATTGAAACATGAAGAAGAAGACCCCTGCAGTTAGCAGTTGCCAT  
TAAACAGGAGCCGCTTGATGCAAAATATCTTCAATGGTGTCTGCAAGGCTCTGT  
GGGAGCTACTGTAAATCAGGTAAGCAAAACCAAGAGGTGGCAGCTCCT

CTTCTCCCTCCGTCCCTTTTCCCCCTTAGGGCTACATACAGATCACTTTTGTG  
GAGCCCTACCTTGATGAGTATGAGATGAAAGACAGGGTCACATACCTTGAGAAGA  
ATTICAACTCCGGAGGTTATGTATACCACCCCGTTCAACCTGAGAGGG  
GCGGCTCCGGGAGAGCTCCATGAGCAGTACAGAAGGAACACAGTCTCTGAC  
CACTATGTACGGCTTCCCTTACATCAAGACTAGGATCAGCGTCACTCCAGAAG  
GAGGAGCTAATCCACCCAAAGGATGGGCACCACTTGATGAGT

FIG. 7A (3 of 4)

21st exon (nucleotides 62398 to 62568)

TCATTTATTTCTCCACACTGATATTTTCATCTCAGATGTGGTGAAGCTGTAG  
AGAAAAACAAGCGTCTCATTCACGGGAGAGGGAATATCAGCAGGAAC  
TCAAAAAAGAACTATAACAAGCTAAAAAGAGAACCTCAGGCCAATGATCGAGC  
GGAAAAATTCCAGAACTGTACAAGCTAATATTCAGAGTTGAGAGTCAAAAAG  
CTAAGAATAGGGGACAGAGGAGGCTCTCTCCTCTGGGAT

22nd exon (nucleotides 63040 to 63294)

CCTCCCTCTCTTTTCTTAATTTTCAGGGACTCCTTCCACAGATCTAGTTTCAGGA  
AATGTGAAACCCAGTTGTACAGGGGAGCTAAGAAAAAGCCATCTTTCATTCTGT  
GGAGACTGTGGGCTCTGAAACCTTGGAGAAAGGACTTGCTGGTACTTAAAAAAT  
GGGACATTTGGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTC  
TGGAAAGCTTTGGGATCCCAAGAACCATGGAATTATTCCCAAATGGACTCTGA  
CCAGATITTTGGCCATACTGGGGGGGTGGGGGGGATGGAGGATGGGTACTCAGGC  
ATGACTGGGTATTTATTAAAGTGTGTTTTTCCACAATGTACCAAACAAGGCAT  
AAGCAGCTTCTCCTGCTGACTGGCCCAATCACTGCCCATCTGAGAGATGATTTT  
CTCTGGGCCATATTTGAATTTATTGGAGTAACTCAAATTGCCTGAGGAAAAAT  
GGAAAAATTATCCACCAGTCGATTCAAACTGAATTTCACTCTTTATAGGAAG  
GCAGGGCAAACTTGTAGGAGTACGAAACATTTTCAATAAATCTACAAAGGGA  
AGCCTTACACAAATTCAAAAAATCATCATGGTTGGAAATTTGGGAGGAGATT  
ATTTGTGAACTTGTTACCCCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTAT  
TTTTGTCTTTATTATTACTGTACATTAATTTAACATGCATTTATAGAAGAATAC  
ATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAA  
ATCACAGATACTGCTTTCACTTAAATGGAAACAATTCTCCGATAATGCTTTGC  
TTTTTTTTTTATGTCACTCTTGTGTACTATCTATTTTTCTCCTCTCTGGGACCAA  
GTTTCTTTTTTATAAAGCAATAATATCTCTGTTTTTCATTTTCAGAACATTGTGCTG  
TCTGTACGATATGTATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTG  
ACAAAGCACTTTAGGAAAAGGAGGAACAAAGACATTATTGAGAATTAAATT  
ATATATTTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAA  
TTGCAAGCTAAAAA





FIG. 7B (2 of 15)

















FIG. 7B (10 of 15)







FIG. 7B (14 of 15)

FIG. 7B (15 of 15)

GGAACAATTTCTCTCTATGTGTATGGCTCCCTAAAGTGTGGCTGAGCATTGTCCACATGGGTG  
 ATGAAAGGATCACTAACTAGGAGGASTTGGGAAAAATACAATCATGGGAATTCCTGTAGC  
 ATGAAATGTGTATAGGASSTAGAAATATTCATACACAGSTTCCTGGTGTTCCTGTGTGTA  
 GAAACASTCAGCCAAAAAGGTTTCASTGTGCTTGAAATGAGAATGGGTGGATCAAAATGGCAGT  
 CATGATTTAAAGGATTTAGTCAGATACAGACATCCTCACATASAGAAAACTCTGAATGGCTG  
 GGGGAGAAGGAGTCAAATGCCCTGGATCTTTTTCTTGGGCTCAAAGTCTCTCTCTCTCATCA  
 TCTTCCAGTATTGGGAGGACCTGAGTGCAGGCATCATGGCTCTGTAACTTCACAAGGGTA  
 TGTATTATCTGACAAAACTACGATGTCCACTAACAGGCTACTGAAAGSTATCTTAGICAGTTC  
 TGGTCATTGGCCAGCTAAGGCCAACSTTTTATAACATGATATCAAAGAATGCATCAAAAATTGT  
 GATGATTTCTTAAAAATAATCATTTTATTAGATTTTCTATTTTAAATCAAGGTAATTTTACG  
 GAAATAAGGAAACASTTACTCTCCACCAAACTTGGGAGTADCAAGACAGAGATAAGT  
 ACCCTCTGGCTTCCCCTCTCTTCACTAGTAAGTATGASTTCCAGTCTTACTTAGGCAATGGTCA  
 AGTSCAAAAGTGGCCAGGGTATGIGTTTGGCTCTCTGTCTCTTAGADCTCTCTACCATCACTCA  
 CATCTCCAGTCAACAGATCTCTAATCTCTGTGACTSTGTCTGGACATCAAGACAATACTCTCTCT  
 CTCTCTGCCAACCGTACTTAAAGGTATATAAAGAACCTCTGGGABCTGTGGTTTGTATGTCTC  
 TAGACTAGGTGGGCTTCCAGGTGACTGAGTCTCATCCAAATTAAGGTTCATATTTGGGGAGAA  
 GGGGTAGCCCCAAAACTTACCACCATTTGTAGTATGCATTTTTTTGGAAAAGCATATTCAAAA  
 TCTGAAATGCCAAGTTACAGACCTCTTTTTGTAAAAATAATTTTGTGCTAGTATAATTTACAT  
 AIAATAAAATTCACACATTTTAGGTGTACAATTTGGTGAACCTTGGGCAACTTAGAGTCACTTAA  
 CCTTTCTCTCAGTCAAGATATAGAACACTCTTTTTATCTTAAAGCTTCCAGGCGCTCTTAC  
 AATCTCTCTCTCCCCAGGCCACACCTCTCAACTCAAGCAATCTCTGACCTACTCTCTCTACATA  
 ATTTTGTCTATCTGGAGCTTCAATATCTCTGTACAGTATGTACAAACCTCTCTTTTGTGAGACA  
 GGGIGTCAGTCTGTACCCAGCTTGGAGTACAGAGGTGTGATCTTAGCCTACTGCAACCTCAAC  
 CTCCAGGATCAGATGATCTCTCTCTCACTCATCTCTCAAGTAAGGGGAGTACAAGGAGAT  
 GCCACACACCTGGCTAATTTTTGTACTTTTGTAGAGACAGGGTCTCTGCTATGTTCCAGG  
 CTGCTCTTGAACCTCTGGGCTCAAGGATCTCTCTGCTCAGCTCTCCAAAGTGTGSGATTAC  
 AGTSAGCCACTGCACTGGGCTTAAACCTTCATTTTTTAAACACATTTCTCTTAAATTTGAAGA  
 TTGGCTACATTTTTATATCAATGCCAATTTGTGAGTGTGGCTATATGTATTATATTTTACAGC  
 ACTAAATGCCAGATGTGTGCCAAGTGAGATAAATCTGACAAATGAGATGTTTGTAAACCCAGC  
 AGTGAATAATCACTTCTCTGTGAGAGAGCTCCAGCCCTCTCTGATCACTTCTCTCAACAGCA  
 CAGCAGCACTCTTGTGGTTCTGCTGCTTATCTTGAAGAGGTTAGGTTACTTTTTTGTCTACT  
 TATTACTTCGAAACCACTTCTGCTTAGAAATTTGTAACTTCTCTTCTAGTTTCGGTAACCG  
 CCATTTTGTCTCTCTGTAACAATTTACGCGCGGTGTAACCTGTGAATCTTT

FIG. 7C

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hCLASP4 -----MFPMEDISISVIGRQRETVC----- 20
hCLASP5 -----MTHINSLOWDLAQELG----- 16
hCLASP3 -----MAERRAFAQKISKVAAEVREHQISSQYSGSPQLKLNINVG 41
hCLASP2 -----MLLFYDDFQTALRRQGEVICS----- 23
hCLASP7 -----MAASERRAFAHKKINRTVAAEVRFQVSRERSGSPHSSSRCS3SL 43
hCLASP1 MSFRGKVFKEPSEFWKKRRTRRVIQEEFHRESSQENPILLEPLDYETVISELEKTYEN 60
      . . .

hCLASP4 -----STVTHDAEKPAQSLFVNECIKTYSDWHVYNK 53
hCLASP5 -----DHT 19
hCLASP7 N-----LSHHTTVPLTHAYCPVDLEDYLTTHPLAVDSGFLHDLNKP 85
hCLASP2 -----TVPAKAEEREAQSLFVTECIKTYSDWHVYNK 53
hCLASP7 G-----VPLTEVVEPLDFEDVLLSRPPDAEPGFHDLNKP 79
hCLASP1 DPLQDILLEFPSSDDFSAACVSWDIRTLYSTVPDAEKHAENILVFEACHFYSSQWHVYNK 110
      . . .

hCLASP4 YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEECEHDED-----SSSLCNQEGGVIRKGS 105
hCLASP5 DDDLDVVVETPKFCRTLAP-SLPEECVELEPHVR-----DDWQTYIRRWL 63
hCLASP3 PDDIEVVYSPFDCRTLMS-AVPEE-SEMDPHVR-----DCISFYTLDWAL 126
hCLASP2 YEDYSGEFRQIPNKVWHLQHLFVHVVEVDEEVDHDED-----AASLSQEGGQITKGS 107
hCLASP7 ADDIELLLQPRECRTHP-GIPKD-EKLDQVR-----AAVENIIFWNI 127
hCLASP1 YEQYSGDIRQLPRAEYKPKHLPSHSFEIDHEIAIKDEETTSHS SKGGG GAGGIGVFNK 186
      . . .

hCLASP4 WLEKANVNSTIT--VTHMVFHFRYFYLTLEDSYILNSYDEPNKSKESK-GCIYLDANI 161
hCLASP5 VNRKNQGSPEIC--GFHYETGSKEDFHKT-LEHQTFESETLECSI PAAQA--GFPHLWIC 118
hCLASP3 VIRKYNH LGTGF--NHTILDEQHERQKG-LEHGVFESEEAIDGMSYQDDQDIPRSHNI 180
hCLASP2 WLYKGNMNSAIS--VTHMVFHFRYFYLTLEDSYILNSYDEPNKSKESK-GCIYLDANI 164
hCLASP7 VHERYQYLSAAY--GFWTDDTQERQKG-LEHGVFEQDASGDESGPEDSNDSRGSORP 179
hCLASP1 WLYKGNFNSTVNNTVTVNRSPHFRYFQLTQLPLNISYIMNFYDEPNKSKESK-GCIYLDANI 239
      . . .

hCLASP4 DVVQCQPMRPHAFELMNDLYSHYLAAEIEQEHEEWLITLKHIIQINTDSIVQERFTE 221
hCLASP5 DVSGGQPVTAQDFELMLQFDEKLENLLQVSAEDFEKQNEARETN-----FQAE 169
hCLASP3 DDTPRGSWAGSIFDMLSLIDALLPNLLDKTPNEEIDRQNDQQRKSN-----FHKAE 234
hCLASP2 GVMQNNKVRFFAFELMNDLYSHYLAAEIEQEHEEWLITLKHIIQINTDSIVQERFTE 221
hCLASP7 EDTPRSGASSIFDMLSLIDALLPNLLDKTPNEEIDRQNDQQRKSN-----FHKAE 234
hCLASP1 GVMQNNRLRKYAFELMNDLYSHYLAAEIEQEHEEWLITLKHIIQINTDSIVQERFTE 221
      . . .

hCLASP4 TAQDDETSS---QKKAENIMASLERSMHPFLMKYGPTEFQINKLSPGDGRQNLFPFDSH 278
hCLASP5 LEALYERVT---ELQVVEIRPYPECPKEHLG-----N-----SILVPLTLFENIE 211
hCLASP3 LEALYERVT---ELQVVEIRPYPECPKEHLG-----N-----SILVPLTLFENIE 211
hCLASP2 ENHDEPFI---FLQVVEIRPYPECPKEHLG-----N-----SILVPLTLFENIE 211
hCLASP7 ENHDEPFI---FLQVVEIRPYPECPKEHLG-----N-----SILVPLTLFENIE 211
hCLASP1 ENHDEPFI---FLQVVEIRPYPECPKEHLG-----N-----SILVPLTLFENIE 211
      . . .

hCLASP4 WKLDPS---GIEHDIHP-FEEKONKRFVNVHDLTFNILGQIGDNAKGPHNVEPEFI 335
hCLASP5 IEPLEAS---IALNDVKKERKKISENFHCDLN:DQKGFLEAHTPSVAASSQARSASVSV 268
hCLASP3 IEPLEAS---IALNDVKKERKKISENFHCDLN:DQKGFLEAHTPSVAASSQARSASVSV 268
hCLASP2 ALEHLEF---JAFHEVYT-FFEFHGRILUKHNLGFNIYVVAENREGFTTNVEPEFI 335
hCLASP7 IEPLEAS---IALNDVKKERKKISENFHCDLN:DQKGFLEAHTPSVAASSQARSASVSV 268

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FIG. 8 (1 of 6)



hCLASP4	NLAIFEVFNKIKIAI FHVILNEFSEVREMLWGSSTQLASDGSP---KGSSEPSYIHGIAE	390
hCLASP5	TYPSDDIVLVKIEKVLQGGD----IGDASPPYTVIKS IDG-----GKSHE-KIEKLL	397
hCLASP3	TYPSQDVLNLIKRLKRLQGGD----IGDASPPYIMIFKRLDA-----TKN-E-ALEKLLS	382
hCLASP2	TLSLEFDIKYNKRI SADPHVDLNHFSVPQMLATTSFALMUGS-----GQD-SVANGILHE	381
hCLASP7	TYPSDDIVLVKIEKVLQGGD----IGDASPPYIMIFKRLDA-----TKN-E-ALEKLLS	378
hCLASP1	SVALYDLASGRKISADPHVDLNHAAVRQMLLGASVALENGNIDTITPRGSEPHIKOLPE	479
* * * * *		
hCLASP4	SNIRVIIGGIESVTPNPHPIELVARIEKVLQGNITHCAEPIKNSDPVHTAQKUHRTAKQ	450
hCLASP5	QAESDQLR-----LGRIRMPFAWAPISLASFPPWSTLERETDVDSMVGR PVGRKRTLA	372
hCLASP3	QADQPCQR-----LGRIRMPFAWATATHMINIVISAGSLHRDSTEVEISTGIRKSWDEER	437
hCLASP2	AAMQYPRNGIFSVTPNPIELFIMARIEKVLQGNITHCAEPIKNSDDSSHLAQKILKNARQ	441
hCLASP7	AADQPCQR-----LGRIRMPFAWATATHMINIVISAGSLHRDSTEVEISTGIRKSWDEER	429
hCLASP1	EWLAFPHLAVESV INPHSHIVIAKIEKVLNENIASGASPIKNSDPVHTAQKILKNARQ	539
* * * * *		
hCLASP4	VGSRLGIRMPFAWAPISLASFPPWSTLERETDVDSMVGR PVGRKRTLA	510
hCLASP5	QSRRLSRAALSLDHNGVGSNPKTL-----TLNLSSEFFKQEDFLSDEDLPFLADYKASS	427
hCLASP3	NSSIVGHSLEHTTSGDDACNITLFR-PATLTITNFFKQEDFLSDEDLPFLADYKASS	496
hCLASP2	ACQRIIGIRMPFAWAPISLASFPPWSTLERETDVDSMVGR PVGRKRTLA	501
hCLASP7	---RRSPQ---DRAASGDDACNITLFR-PATLTITNFFKQEDFLSDEDLPFLADYKASS	483
hCLASP1	FGSKLGGIRRAFAWAVRSVDFINQGVDRDSEKIPFLFRQELSPISTEDLVLVDFYKAD	599
* * * * *		
hCLASP4	--KTHLDQIPGVLNITWECVVDLNCITSSSYPLKPPF--FNQONITVEVSEFPENTKY	567
hCLASP5	SLQREVEIPGLDELEISWAFELINCCITPHILPVKPPF--ENFTFPRKELEFI--TFEV	484
hCLASP3	SVLRREHITAQLHIDISPAFEMHYCLPPELLQVKLY--DSFVPETRELEFI--ASEV	553
hCLASP2	K-MAKLEILGHLIDITDINVSDEFNYNSSVIRTKQFETCSFTETELVLEFVPCIKH	560
hCLASP7	SLRREHITAQLHIDISPAFEMHYCLPPELLQVKLY--DSFVPETRELEFI--ASEV	560
hCLASP1	K-ISPHTQIPGLHIAIDINVSDEFNYNSSVIRTKQFETCSFTETELVLEFVPCIKH	558
* * * * *		
hCLASP4	CNEFTLFINHLAVPIQLHYDSQRTAFARNIAVCEFFDADESIASALFIYGRHDSV	627
hCLASP5	YAPHTSYINHLAVPIQLHYDSQRTAFARNIAVCEFFDADESIASALFIYGRHDSV	541
hCLASP3	YAPHTSYINHLAVPIQLHYDSQRTAFARNIAVCEFFDADESIASALFIYGRHDSV	610
hCLASP2	TQPYTICCNHLAVPIQLHYDSQRTAFARNIAVCEFFDADESIASALFIYGRHDSV	620
hCLASP7	YAPHTSYINHLAVPIQLHYDSQRTAFARNIAVCEFFDADESIASALFIYGRHDSV	597
hCLASP1	CRPYEVEINQIYAPHTSYINHLAVPIQLHYDSQRTAFARNIAVCEFFDADESIASALFIYGRHDSV	718
* * * * *		
hCLASP4	FTTNAAVAVSHHNQNEFFYDEIKIHLPIHLHQHLLFTFYHVSCEINTHCTTHQITVE	687
hCLASP5	FLQEVYTAVTYHNKSEDEFBEVKIELPAHLTVIHLLEFTFYHISCCQ-----FQGASVE	595
hCLASP3	FSKEAYTANTYHNKSEDEFBEVKIELPAHLTVIHLLEFTFYHISCCQ-----FQGASVE	664
hCLASP2	FTFSAAAVVHHNQNFFYTHKELFELTILHHLHLLFTFYHVSCEINTHCTTHQITVE	687
hCLASP7	FTFSAAAVVHHNQNFFYTHKELFELTILHHLHLLFTFYHVSCEINTHCTTHQITVE	651
hCLASP1	FTFSAAAVVHHNQNFFYTHKELFELTILHHLHLLFTFYHVSCEINTHCTTHQITVE	705
* * * * *		
hCLASP4	FWGFAWVPIKELGHIITFRQQLPAGANIPGYNILNDAESFPQCNVITRAVDCAHLLK	747
hCLASP5	TLLGYSWLPIILNERLQTSSYCLPVALEHLPNYSMHSAEKVPLQNEPIKLAEGHRGVFN	655
hCLASP3	TPVGTYWIPMIQNGRIKTCQCLPVGLEHPPQAYSVLSPEVP---LFGKRWVDNHRGVFN	721
hCLASP2	TQVGYSWLPIIKDGRVITSEQHIPVSANLPSGHLGYQELGMGRHYGPEIKWVGGKPLK	740
hCLASP7	TPVGTYWIPMIQNGRIKTCQCLPVGLEHPPQAYSVLSPEVP---LFGKRWVDNHRGVFN	739
hCLASP1	TPVGTYWIPMIQNGRIKTCQCLPVGLEHPPQAYSVLSPEVP---LFGKRWVDNHRGVFN	734
* * * * *		

FIG. 8 (2 of 6)

hCLASP4	FESHLESTIYTQELHWHKFFHHNQLIQS-----SSKEWIGELIKYLSKLHAM	784
hCLASP5	IEVQA'SSVHTQENHLEKFFTLDSLESVTFEAFVLTQKISEMALEHEHLKLSIICLNS	715
hCLASP6	NEVVA'SSHTQDPYLERFFALYNALDER-LFFVRIQEMRIMENNELNELSSISALNS	769
hCLASP2	ISTHLS'STVYTQDQHLHNFQYQCKTES-----GAQALGNELVYKLSKLHAM	787
hCLASP7	VELTA'SSVHPQCPYLERFFTLVHTLERG-AFPFELKDV'LEEGN'EQELKASLALIKLA	767
hCLASP1	VSTFV'NST'NTQDPHYNAFFQECQKREH-----MQSPSTSNFIRSCENLLNYS	887
.. * : * : * : * : *		
hCLASP4	ELQWMIQELPV.LMQLEF-----VLTIMTH-----EDDVP	824
hCLASP5	RIEPLVLEFLHVLKHLFQLSVQPMVIAGQTANESQFAFVVAIAIANSLHN:KDLH:DQH	775
hCLASP3	QLEPV'RFELHLL'KLILLV.RFPVIAQCIVNLGQAFBAMASIINRLHKNLEGN:DQH	849
hCLASP1	HGHVMIAPLPT.LMQLEF-----VLT-RAT-----DEEVA	816
hCLASP7	SHEPLVAFSHHVLRKLVLELVRPPIISGGIVNLGRGAFHMAHVVLVHRSLEAAQDAR	827
hCLASP1	KTHAINSELPILMQLEF-----VLVQNE-----EDBIT	916
. : * : * : *		
hCLASP4	INCTMV-LLHIVSFCHEEGLDS-----VLRSEIFHS-----EPPEP	860
hCLASP5	RNCLLASVHYVFLPEVQRDVPSGAPTALLDPRSYHTAGRTSAAAVSSLLQAVMS	835
hCLASP3	RNSILLASVHYVFLPNIYPNSSSPG-PGGLGGSVHTATWASAVIPASLNELN:ELHSE	899
hCLASP2	VNVTRV-ILHVVAQCHHEGLS-----ELKSIVETA-----PAEPT	852
hCLASP7	HCPQLAAYVHYAFELPGTEPSLPDGAPP----VTVQAATLARGSGIPASLYLAR:ELHSE	883
hCLASP1	TTVTRV-LPDIVARCHHEQLDH-----SVQSYIFEV-----FETRAQ	852
. : * : * : *		
hCLASP4	SAPQAQLIH-----ETLATTNIAILFQS-----	883
hCLASP5	SNPDLAGTHSAADHEVENINMSKIDRNCSSRM:SYVCGSLDAPSSFA-----	882
hCLASP3	SNPDISGTPTSPDDEVRSIIIGSEGLDRNSWVNTGGFKAAPWGSNIPSPAESTQAMIRSC	959
hCLASP2	VASEYKTVH-----ELTHSNNTIILKPS-----	875
hCLASP7	SNPDLAVALPGSVDEVSFILASKLHEELA-LQ-----	915
hCLASP1	KE---RPVH-----ELARNVTGLIKSN-----	872
. : * : * : *		
hCLASP4	-----ADFLSINKLLKYS-----WFFFEILAKSM	907
hCLASP5	-----AERPASKEHPHEELALQ-----MVVSTIGIVFHS	910
hCLASP3	NRMSSHTETSSILQTLTGRLPTRLFLHEELALQWVVGSGVRESALQQAWFFFEILMVFS	1019
hCLASP2	-----ADFLTSNKLLRYS-----WFFFDLILFHS	899
hCLASP7	-----WVVSSEAVREAILQHA-----WFFFEQLMVFS	942
hCLASP1	-----DSPTVPHVLKHS-----WFFFAILKSM	995
. : * : * : *		
Cacharin Cleavage		
hCLASP4	ATVLLLENF IKLERGQFFPEPTYPHVLHSLLLATIPHVTIRYAEIPDE---SRNVVYELAI	964
hCLASP5	AQHVHNMDFRDSEFRTFSDRFMDITTIVNVVTSEIAALIAKPKQENEQAEMN:ISLAF	970
hCLASP3	UHHLYENDLEAIFKSEFPERENDSIAALVSTIASEIVFICRDTM---VERLNTSLAF	1070
hCLASP2	APHILFNDFVKLIENQEFEPACYHHAARTVGMNIPRITIKLGRNPHA---CKNAI:RSLAF	970
hCLASP7	ALHLLIQELNTHKLEFEGRELSCITALVGSVGLVITFMKEVEL---AELINAILAF	999
hCLASP1	ALHLLITNFIILSEFEPFYNELINVMN:CEVIMK:PIALER---TSFATROVAF	1001
. : * : * : *		
hCLASP4	FLHRLTINDFGFLENINDYISFSFKDF-----KVLAEYKFEFLATIGNHEHVIPLNL	1019
hCLASP5	FLYDLISLNDRGFVENIRHYCSQISAKLSNL---PCLISMRELEFLRILCSHEHVIPLNL	1017
hCLASP3	FLNGLDSVNDRGFVRSIIKSYQVSSKLYSLNPSVLVSLRLDPLRIICSHEHVIPLNL	1106
hCLASP2	FIKRYFTENDRGFVFAGINNYISCFAPGDF-----KILFEYKFEFLVVCNHEHVIPLNL	1011
hCLASP7	FLSDI:ELITSEFVENIVRAHYQVATRLQSHNPAALTLAMEFTRILCSHEHVIPLNL	1099
hCLASP1	FLKRYFTENDRGFVFAGINNYISCFAPGDF-----KILFEYKFEFLVVCNHEHVIPLNL	1107
. : * : * : *		

FIG. 8 (3 of 6)

FIG. 8 (4 of 6)



ITAM

hCLASP4	ERFGTENVKIIQDSDFVNAKELDPHNAHIQV	VKEVFDDKELTERKTEFFERNHNISRFV	1799
hCLASP5	QFPGAEFVEVIKDSDFVNAKELDPHNAHIQV	VEVFDEYEMKDRVTYFEPNPNLRPFM	1810
hCLASP3	ERFGEDVVEVIKDSDFVNAKELDPHNAHIQV	VEVFDEYEMKDRVTYFEPNPNLRPFM	1930
hCLASP2	DEFGLENVEMIQDSGKVNPAIILISDAI	IQVTVIHFDEKELQERKTEFEFSHNIRRFM	1770
hCLASP7	ERFGDDVVEVIKDSDFVNAKELDPHNAHIQV	VEVFDEYEMKDRVTYFEPNPNLRPFM	1851
hCLASP1	DEFGADNVKIIQDSDFVNAKELDPHNAHIQV	VEVFDEYEMKDRVTYFEPNPNLRPFM	1972

ITAM

hCLASP4	FEAPYTLGGHKGCGIEEQQRRTILITNSHF	VKEVFDEYEMKDRVTYFEPNPNLRPFM	1859
hCLASP5	YTTPTLEGGHKGCGIEEQQRRTILITNSHF	VKEVFDEYEMKDRVTYFEPNPNLRPFM	1870
hCLASP3	YCTPTLEGGHKGCGIEEQQRRTILITNSHF	VKEVFDEYEMKDRVTYFEPNPNLRPFM	1992
hCLASP2	FEMPTTCTGKHQSSVEEQQRRTILITNSHF	VKEVFDEYEMKDRVTYFEPNPNLRPFM	1830
hCLASP7	FCTPTTCTGKHQSSVEEQQRRTILITNSHF	VKEVFDEYEMKDRVTYFEPNPNLRPFM	1911
hCLASP1	FETPTTCTGKHQSSVEEQQRRTILITNSHF	VKEVFDEYEMKDRVTYFEPNPNLRPFM	2032

Coiled-coil

hCLASP4	RTAEQLKLSSTIDVLAQLKLGWVSQVNA	SELAIAFAFINDSQASKYPFKVSELR	1919
hCLASP5	RTAEQLKLSSTIDVLAQLKLGWVSQVNA	SELAIAFAFINDSQASKYPFKVSELR	1930
hCLASP3	RTAEQLKLSSTIDVLAQLKLGWVSQVNA	SELAIAFAFINDSQASKYPFKVSELR	2052
hCLASP2	RTAEQLKLSSTIDVLAQLKLGWVSQVNA	SELAIAFAFINDSQASKYPFKVSELR	1890
hCLASP7	RTAEQLKLSSTIDVLAQLKLGWVSQVNA	SELAIAFAFINDSQASKYPFKVSELR	1971
hCLASP1	RTAEQLKLSSTIDVLAQLKLGWVSQVNA	SELAIAFAFINDSQASKYPFKVSELR	2092

Coiled-coil

hCLASP4	EMERKEFIQACSI	FALENNERLIKELQVEYHEGLEK	NFRIMVHELSDI	IHEQILQEDTMHSP	1979
hCLASP5	LCFFKEFIMRCSEAVEFNHRLITAI	QREYQDELHN	NHNLHENLRPM	IERKIPELYAPIFR	1990
hCLASP3	LCFFKEFIMRCSEAVEFNHRLITAI	QREYQDELHN	NHNLHENLRPM	IERKIPELYAPIFR	2090
hCLASP2	EVFFQFVEACG	JALANERLIKELQVEYHEGLEK	NFRIMVHELSDI	IHEQILQEDTMHSP	1949
hCLASP7	LCFFKEFIMRCSEAVEFNHRLITAI	QREYQDELHN	NHNLHENLRPM	IERKIPELYAPIFR	2030
hCLASP1	EIERQFADACG	QALDYNERLIKELQVEYHEGLEK	NFRIMVHELSDI	IHEQILQEDTMHSP	2152

PTM ligand

hCLASP4	WMNTLHVFCALSGTSSDRGYGSE	YAEV	2008
hCLASP5	VESQKRDSFHRUSFR	CETQLSQG	2015
hCLASP3	VLPNLSLHIFNAISGTSTMTVMHGM	SSVV	1980
hCLASP2	--PGLRNSINP	SFRADL	2047
hCLASP7	GVDQTCSTRVISHATPALPTV	SISS	2180

FIG. 8 (6 of 6)